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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ado50295 Escherich	ADO50295	12	1901	97.2	1284.6	18
Adl16137 Escherich	ADL16137	12	1299	97.4	1287	17
Aca19297 Prokaryot	ACA19297	8	1299	97.4	1287	16
Abk12514 DNA encod	ABK12514	ω	1299	97.4	1287	15
Aee75418 E. coli B	AEE75418	15	1901	97.4	1287.8	14
Aed50819 Escherich	AED50819	14	1901	97.4	1287.8	13
Ado50297 Escherich	ADOS0297	12	1901	97.4	1287.8	12
Adc87744 DNA encod	ADC87744	10	1901	97.4	1287.8	11
Ada19449 E. coli K	ADA19449	œ	1901	97.4	1287.8	10
Aad25463 Escherich	AAD25463	σ	1901	97.4	1287.8	9
Ado50303 Escherich	ADOS0303	12	1323	99.5	1315.6	8
Ado50301 Kangaroo	AD050301	12	1323	99.5	1315.6	7
Aee75412 E. coli B	AEE75412	15	1323	100.0	1322	6
Ado50291 Escherich	AD050291	12	1323	100.0	1322	u
Ada19445 E. coli B	ADA19445	8	1323	100.0	1322	4.
Aad25460 Escherich	AAD25460	0	1323	100.0	1322	ω
Aad36473 Escherich	AAD36473	σ	1323	100.0	1322	N
Aac88885 Escherich	AAC88885	v	1323	100.0	1322	_
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AED50824	ACC57673	AAD06832	AED50817	AEE75422	ADA19452	AAD06831	ACC57672	AAA28216	ABB75420	ADO50299	ADC87742	ADW76362	AAC68299	AEF15218	ADL16138	ADL02197	AAC68294	AAC68300	AAC68295	AAC68297	AAC68296	AAC68298	AEB75417	ADO50296	ADL16139	AEE75416
Aed50824 Escherich	Acc57673 Escherich	Aad06832 E. coli a		2	Ada19452 E. coli K	Aad06831 E. coli a	Escheric	M		Ado50299 Escherich		Adw76362 Phytase A	ຜ	Aef15218 Escherich	Adl16138 Shigella	Adl02197 DNA encod	Aac68294 Lama2/APP		Aac68295 R15/APPA	Aac68297 R15/APPA		R15/APPA	Aee75417 E. coli p		Adl16139 Shigella	Aee75416 E. coli p

ALIGNMENTS

RESULT 1 AAC88885 30-NOV-2000. 07-MAR-2001 (first entry) 25-MAY-1999; 99US-00318528. 25-MAY-2000; 2000WO-US014846. WO200071728-A1. Escherichia coli. nutrition; ds. Escherichia coli B; phytase enzyme; anabolic; phytate digestion; Escherichia coli B phytase enzyme nucleotide sequence AAC88885; AAC88885 standard; DNA; 1323 ₽₽.

WPI; 2001-112081/12. P-PSDB; AAB37892. Short JM, Kretz KA; (DIVE-) DIVERSA CORP.

Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from the phytates.

Claim 2; Fig 1; 147pp; English.

The present sequence encodes a phytase enzyme from Escherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate on phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients



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TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACTGG
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                                         TTGACGCCCCATCCACAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG
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The present invention relates to novel dietary aids comprising sustained release biocompatible composition which comprises an agent (enzymes such as phytase, amylase, esterase, protesse) that assists in digestion. The biocompatible composition is effective upon oral consumption and release in the digestive tract of a subject. The dietary aids are useful for delivering enzymes, therapeutics, medicine and agents to an organism. The

Disclosure;

Fig 1; 89pp; English.

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Matches 1323;
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                                                                                                                            GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                  New bacterial phytase for e.g. improving the nutritional value of phytate containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; nutritional value; feed treatment process; thera; thermal tolerance; growth performance; alcoholic drink; biopulping non-alcoholic drink; biobleaching; B phytase; ds.
                                                                                                           WPI; 2002-083108/11.
P-PSDB; AAE15806.
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The patent discloses recombinant bacterial phytase from Escherichia coli CC K12 appA phytase. The enzyme has phytase activity and improved thermal CC tolerance when compared with wild-type phytase. It has improved protease CC stability at low pH. The recombinant phytase is useful for improving the CC improving the growth performance of an organism that consumes it, in CC treating animal digestive systems, in feed treatment processes and for in CC vitro purposes related to research, discovery and development. They are CC also used for generating recombinant digestive systems for CC the use of moulds, grains and/or plants, in biopulping and bio-bleaching CC where a reduction in the use of environmentally harmful chemicals that CC are traditionally used in the pulp and paper industry is desired and in CC thus increasing the amount calories and nutrients present in the feed. The present sequence is a DNA encoding E. coli B phytase protein
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Matches 1323; Conservative
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The invention relates to an isolated Bscherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids condition from W68B, Q84W, A95P, X97C, $188E, R180Y, N226C or Y277D. CC Also included the E. coli appA gene ADA1945 (or an oligomucleotide derived from it) or its mutant sequence ADA1945, expression vectors, containing foodstuff by contacting nutritional value of a phytate-cc containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytase in the phytate containing a microbial phytase (comprising culturing the plant cell, plant part or containing a foodstuff), a method to produce an animal feed containing a feed composition where the nucleotide sequence is expressed and containing the plant cells, plants or plant into a composition for animal feed), a feed composition for animals (comprising the plant seeds, plant cells, plant parts or plants in admixture with a phytate-containing comprising administering to the human or an animal able to benefit from comprising administering to the human or animal the plant seeds, plant cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence containing a phytase enzyme, a transgenic non-human organism whose genome containing a phytase enzyme, a transgenic non-human organism whose genome containing phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The containing the plant end of phytate rich ingredients. The present end of the produce and protease stability. It can be added to the phytate rich ingredients. The present end of the produce of the phytate rich ingredients. The present containing the phytase.
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25-MAY-1999;
25-MAY-2000;
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O' Don
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) KRETZ K A.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
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RADSULT 11
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RW 1
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Short JM,
Mather EJ;
                                                                                                                                                                                                                                                          Claim 3;
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(GRAY/)
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)B; ADO50292.
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BARTON N R.
GARRETT J B.
O'DONOGHUE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATHER
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214. .216
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dough; baking; gene; ds.
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pharmaceutical; fertilizer; cramp; cell culture; osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1323; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1323 BP; 323 A; 353 C; 357 G; 289
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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expression the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease ct improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC improve the feeding value as pigs, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                        Producing phytase, involves providing nucleic encoding polypeptide having phytase activity,
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(GARR/)
(ODON/)
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13-APR-1999;
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KRETZ K.
GRAY K.
BARTON N R.
GARRETT J B.
O'DONOGHUE E.
MATHER E J.
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13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                      Phytase;
phytate;
                                                                                                                                                     mutation
                                                                     20-JUN-2003; 2003US-00601319
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99US-00259214.
99US-00291931.
99US-00318528.
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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Scherichia coli W phytase mutant DNA. Note: The present CC scherichia coli B phytase DNA ADO50291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 1319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1323 BP; 324 A; 353 C; 356 G; 289 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page; 74pp; English.
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(GRAY/)
(BART/)
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DB; ADO50292, ADO50304.
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE B.
) MATHER E J.
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GCCTTCGCCGGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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                                                                                                                                                                                                                                                                                   The patent discloses recombinant bacterial phytase from Escherichia coli CC K12 appA phytase. The enzyme has phytase activity and improved thermal CC tolerance when compared with wild-type phytase. It has improved protease CC stability at low pH. The recombinant phytase is useful for improving the growth performance of an organism that consumes it, in CC improving the growth performance of an organism that consumes it, in CC treating animal digestive systems, in feed treatment processes and for in CC vitro purposes related to research, discovery and development. They are CC also used for generating recombinant digestive system life forms, for CC producing or manufacturing alcoholic and non-alcoholic drinks based on CC the use of moulds, grains and/or plants, in biopulping and bio-bleaching CC where a reduction in the use of environmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in CC the reduction or possible elimination of the need for mineral CC supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed. CC The present sequence is a DNA encoding E. coli appA phytase wild type
                                                                                                                                                                                 Query Match
Best Local Simi
Matches 1293;
                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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                                                                                                                       ATGAAAGCGATCTTAATCCCATTTTTATCTCTTGATTCCGTTAACCCCGCAATCTGCA
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                                CAGATGCGTGATAAAACGCCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC
                                                                                                                                  CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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              CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
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The invention relates to an isolated Escherichia coli polynucleotide encoding a phytase enzyme appearing as DAA19450 and having amino acids modification from W68E, Q84M, A95E, K97C, S168E, R18DY, NZ2GC or Y277D. Also included the E. coli apph gene ADA19449 (or an oligonucleotide derived from it) or its mutant sequence ADA19452, expression vectors, lost cells, a method of improving nutritional value of a phytate-containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytate in the phytate containing foodstuff), a method to produce an animal feed containing a microbial phytase (comprising culturing the plant cell, plant part or plant under conditions where the nucleotide sequence is expressed and converting the plant cells, plants or plant into a composition for animal feed; a feed composition for animals (comprising the plant seeds, plant cells, plant parts or plant into a composition for plant seeds, plant cells, plants or plant at the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds, plant cells, plant parts or plant into a composition for animals comprising the plant seeds and cells, plant parts or plant into a composition for animals comprising the plant cells, plant parts or plant into a composition for animals comprising the plant cells, plant parts or plant into a composition for animals comprise cells.
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2001;
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) KRETZ K A.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O' DONOGHUE
) MATHUR E J.
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                                                                                                                                                                                                                                                                                                                                                                                                             Fig 7; 62pp; English.
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                                                                                            GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGATCACC
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487

foodstuff), a method to treat a human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzymes comprising administering to the human or animal the plant seed, plant cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence encoding a phytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a polypeptide having phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence represents the E. coli K12 appA gene encoding wild-type phytase.

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                                                                            13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
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99US-00259214.

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2000US-00580515.

2001US-00866379.
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New nucleic acid encoding a polypeptide having phytase activity, useful in improving the feeding value of phytate rich ingredients or as an aid in phytate digestion.

Example 1; SEQ ID NO 3; 113pp; English.

The invention discloses a new isolated or recombinant nucleic acid which CC encodes a polypeptide having a phytase activity. Also claimed is a cc nucleic acid grobe, an amplification primer sequence pair, an expression CC cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the cc nucleic acid, an artisense oligonucleotide, inhibiting the translation of CC acid, a bybridoma comprising immobilised polypeptide and CC a second domain, an array comprising immobilised polypeptide or nucleic acid, a hybridoma comprising an antibody that specifically binds to the CC polypeptide, a food supplement for an animal, an edible carrier and the CC polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, making an anti-phytase antibody, producing a recombinant CC polypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, cell entifying of new or modified CC phenotypes by using real-time metabolic flux analysis, increasing CC thermotolerance or thermostability of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a CC digestive system and processing of corn and sorghum kernels. The phytase catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or CC as an aid in phytate digestion. The sequence presented is the DNA CC encoding the Escherichia coli appa phytase.

Sequence 1901 BP; 474 A; 499 C; 499 G; 428 T; 0 U; 1 Other;

밁 Ś δ 밁 S 片 Ś 밁 Ś 밁 5 묽 8 Query Match
Best Local Similarity
Matches 1293; Conserv 548 361 488 301 · CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 428 368 241 181 308 121 248 188 61 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTCTGATTCCGTTAACCCCCGCAATCTGCA GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 97.4%; milarity 99.5%; Conservative 0 Score 1287.8; Pred. No. 0; Mismatches DB 10; 7; Indels Length 1901; 0 Gaps 360 607 420 547 487 300 427 240 367 180 307 247 60

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          AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; gene; ds.
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TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT

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                                                                                                                            The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to cimprove the feeding value of phytate rich ingredients, and in diet of cumerous animals including mammals, fowls and fishes, commercially csignificant mammals such as pigs, goats, laboratory rodents, commercially csignificant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially fetc., in dough making and baking, in dietary aids for animals. The method composition, higher yields and loading efficiency. The phytase cc incorporated in to the dietary aid is safe for animals. The present of sequence is Escherichia coli K12 appA phytase DNA.
                                                     Matches 1293;
                                                                             Query Match
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
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Mather EJ;
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(KRET/)
(GRAY/)
(BART/)
                                                                                                         Sequence 1901
                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 7; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
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                                                                 Local Similarity
 188
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
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2000US-00580515.
2001US-00866379.
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99US-00259214.
99US-00291931.
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Pred. No. 0;
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                                                               CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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   CAGATGCGT
                                                                                                                                   ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
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The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, f oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also

of an animal

for

Example 1;

SEQ ID NO 3; 104pp; English.

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25-MAY-2000;
24-MAY-2001;
24-MAY-2002;
                                                                                                                                                                                                New isolated or recombinant nucleic acid encoding phytase enzymes, useful as foodstuff, and for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic
3-phytase;
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(ODON/)
(MATH/)
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(KRET/)
(GRAY/)
(BART/)
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13-APR-1999;
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P-PSDB; AED50820.
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GRAY K A.
BARTON N R.
GARRETT J B.
ODONOCHUB B.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MATHUR
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99US-00259214.
99US-00291931.
99US-00318528.
2000US-00580515.
2001US-00866379.
2002US-00156660.
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/product= "Escherichia coli phytase protein"
/transl except= (pos:401. .403,aa:Arg)
/EC_number= "3.1.3.8"
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Query Match
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Matches 1293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1901 BP;
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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(GRAY/)
(BART/)
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
BAUM W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a polynucleotide encoding the Escherichia CC coli phytase appA, which was modified to produce a thermostable protease CC resistant phytase which constitutes the novel enzyme of the invention. CC The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, where the polypeptide is a CC modified sequence (AES'5421) derived from the Escherichia coli K-12 appA CC phytase (AES'5421). The modification of the enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of CC the protein. The specification also claims a pharmaceutical composition, a kit; an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing pollution and increasing complement availability in an environment or environmental sample by degrading environmental phytic acid. The novel enzyme is a dietary CC supplement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful CC environmental sample comprises a soil or a body of water. The immobilized converse of hytase is seful in foodstuffs for improving the feeding value of CC phytase is useful in foodstuffs for improving the feeding value of converse rich increasing the feeding to a solution of the converse of the protein converse of the prote
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phytate rich ingredients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 7; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Formulation useful as dietary supplement for treating, preventing creversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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P-PSDB; AEE75419.
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(first entry)

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ABK12514 standard; DNA; 1299

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Phytase; gene; DNA encoding phytase

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                ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                      CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                                              CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGAGGTGAAACTGACC
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                                                       CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTTACGCAA
                                                                                                              CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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Unidentified

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Query Match 97.4%;
Best Local Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel phytase gene, a recombinant phytase gene and their uses. This sequence encodes a phytase associated protein, described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1299 BP; 317 A; 345 C; 355 G; 282 T; 0 U; 0 Other;
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P-PSDB; AAU77775.
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                                                           AACGTGACTGACGCGATCCTCAGCAGGGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC 600
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/product= "Phytase associated protein"
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Pred. No. 0;
0; Mismatches 6;
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GAAGO	TGTGA	TGTGA	GATAA	GATAA	AGCGAT	AGCGAT	GGTCAC	GGTCA	GGACA	GGACA	CATCC	CATCC	GAGGTT	GAGGTT	CAGTG	CAGTGG	CICCIC	CICCIC	GCCGAC	GCCGAC	GAGAA	GAGAA	GCGTTT
CGCAT	GAGCG	AGAGCG	Accco	ACGCC	PAACAG	PAACAG	3CCGGA	ADDOOR	GATAC	GATAC	CCGCA	CCGCA	GCCCG		BAACAC	AACAC	CAACA	CAACA	AATGT	AATGT	CAGGA	CAGGA	CGCGA
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GTGCA	GCAGG	GCAGG	ATTAA	ATTAA	GATTC	GATTC	GCCGC	GCCGC	GGCAA	GGCAA	GGCGTA	GGCGT	CGCCAC	CGCCAC	AAGTT	AAGTT	GGGAAT	GGGAAT	AACCG	AACCGC	CTGTT	CTGTT	 ACGGGT
STITE G	CATGI	CATGI	TACGO	TACGO	GGTTT	GGTTT	AGGTG	AGGTG	TCTCG	ATCTCG	TGGTG	TGGTG	CCCGT	CCCGT	GCATA	GCATA	GCCGG		TGCGG	TGCGG	ATTAA	ATTAA	 GCTTA
1296	GTTCGT	GITCGI	ceccc		CGCTGG	CGCTGG	GTGAAC	GTGAAC	GCGGCG	909999	TGACAT	TGACAT	TATTAC	TATTGO	ACGCGC	ACGCGC	AGCCGC	AGCCGG	TAAGCC	TAAGCC	CGCAGG	CGCAGG	 ATTTTC
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	GGTTT	GGTTT	GTGAA	GTGAA	CAGACT	CAGACT	TTTGA	TTTGA	GAGCTO	GAGCTO	ACTTC	ACTIC	ATCAAC	ATCATO	TATTTO	TATTTO	GGAAGG	GGAAGG	TCAATO	TCAATO	CCATC	CCATCO	TCAAAC
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Search completed: June 14, 2006, 10:31:32 Job time : 903.103 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Short,J.M. and Kretz,K.A.
Recombinant bacterial phytases and Patent: US 6183740-A 1 06-FEB-2001;
Location/Qualifiers
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Watches 1323; Conservative 0 Matches 1323; Conservative 0 Oy 1 ATGANAGCGATCTTANTCCC	ORIGIN - 100.0% Query Match 100.0%		AUTHORS Kretz,K TITLE Phytase JOURNAL Patent:	K X	DEFINITION Sequence 1 from patent ACCESSION AR130956 VERSION AR130956.1 GI:1411928 KEYWORDS .	RESULT 3 AR130956 AR130956	Qy 1321 TAA 1323 Db 1321 TAA 1323	Qy 1261 ATCGTGAATGAAGCACGC Db 1261 ATCGTGAATGAAGCACGC	Qy 1201 CTGGCAGGATGTGAAGAG	Qy 1141 CAGATGCGTGATAAAACG	Qy 1081 CGTCGGCTAAGCGATAAC	Qy 1021 ACGCTTCCCGGTCAGCCG	Qy 961 TTTATTGCCGGACACGAT	Qy 901 TTGACGCCCCATCCACCG	Qy 841 CGCACGCCAGAGGTTGCC	Qy 781 GATTCACACCAGTGGAAC	Db 721 GAGATATTCTCCTGCAA	661
Pred. No. 0; ; Mismatches 0; ATTTTTATCTCTTCTGATTCC	Score 1:	Inknown" Inassigned DNA"	1 20-FBB-2001;		us 6190897.	N .		ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCACCATCACCATCAC 1320 	TGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260 	CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200 	CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140 	CGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020 	TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960 	GCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900 	GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840 	GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780	
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Short, J.M. and Kretz, K.A.
Phytase-containing foodstuffs and methods
Patent: US 6720014-A 1 13-APR-2004;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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                                                                                         CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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Short, J.M., Kretz, K.A., Gray, K.A., Barto O'Donoghue, E. and Mathur, E. J.
Recombinant bacterial phytases and uses Patent: US 6855365-A 1 15-FEB-2005;
Diversa Corporation; San Diego, CA
                                     GATTCACACCAGTGGAACACCTTGCTAAGTTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                          GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC
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CGCACGCCAGAGGTTGCCCGCAGCCGCCCACCCCGTTATTGGATTTGATCATGGCAGCG
                       GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                         GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                                                                                                                                                                                               GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCCGGGGTGGGGAAGGATCACC
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Short, J.M., Kretz, K.A. and O'Donoghue, E
Dietary aids and methods of use thereof
Patent: WO 0109317-A 1 29-NOV-2001;
DIVERSA CORPORATION (US)
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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AX338966 1 GI:18129102
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ALELMWTLPGQDDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDXTPLSLNT
PPGGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSLRSHHHHHHH"
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                                    CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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Recombinant bacterial phytases and uses thereof Patent: WO 0190333-A 1 29-NOV-2001; DIVERSA CORPORATION (US)
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Enterobacteriaceae; Escherichia.
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5 밁 ঠ 밁 S 닭 ð 밁 Ş Query Match Best Local Similarity Matches 1323; Conserv 241 181 181 121 121 61 61 μ μ ACCTGGCCGGTAAAACTGGGTTGGCTGACCACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTCTTCTGATTCCGTTAACCCCCGCAATCTGCA GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTGATTCCGTTAACCCCGCAATCTGCA 100.0%; ilarity 100.0%; Conservative 0 0 Score 1322; Pred. No. 0; 0; Mismatches 0; Indels 0, Gaps 180 120 300 240 180 60 240 120 60 0

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Short,J.M., Kretz,K.A., Gray,K.A., Ba O'Donoghue,E. and Mathur,E.J.
Recombinant bacterial phytases and us Patent: US 6855365-A 7 15-FEB-2005;
Diversa Corporation; San Diego, CA Location/Qualifiers
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                                      CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                                                             AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                                                                                                                                 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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                                                                                                                                                 AACGTGACTGACGCGATCCTCAGCAGGGCAGGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                                                                                                                     TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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nilarity 99.5%;
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patent US 6855365.
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Pred. No. 0;
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Query Ma Best Loc Matches Qy	FEATURES BOU	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION	RESULT 10 AX356572	Qy db	g 9	gb Qy	d Qq	g Q	D Q	g Q	g Q	g 49	<u> </u>	문
Match 97.4%; Score 1287.8; DB 2; Length 1901; Local Similarity 99.5%; Pred. No. 0; Les 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0; 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTTGTTAACCCCGCAATCTGCA 60	e	Enterobacteriaceae; Esches 1 Short, J.M., Kretz, K.A., Gs O'Donoghue, E. Recombinant bacterial phys	Escherichia coli Escherichia coli Bacteria, Proteobact	AX356572 1901 bp DNA linear PAT 06-FEB-2002 ON Sequence 7 from Patent WO0190333. N AX356572 AX356572.1 GI:18621059		1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300	1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260 	1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200 	1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020 	901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960 	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900	781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840 	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780 	848 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 907
D Q D Q	p Q p Q	QQ 4G	р Q	유 상	B 6	B &	4g V Q	₽ Q	B &	B &	4g VQ	β Q	β Q	gg Qy	4d 6d	οь
1021 ACGCTTCCCGGTCAGCCGGATNACACGCCGCCAGTGGTGATACACTGGTTTGAACGCTTGG 1080	TTGACGCCCATCCACCGCAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900 	GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA	GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600 	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	421 TCCAGTCCCGATCCGTTATTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480 	361 GCCTTCGCCGGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA 360 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGAACGGATTGCTGGCGAAAAAAGGGCTGCCCG 300	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180 	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGGTGATTGTCAGTCGTCATGGT 120	188 ATGANAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 247

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                                                                                                                                                                                                                                                                                                                                                                                                                          group protonation
J. Biol. Chem. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ostanin, K. and Van Etten, R.L. Asp304 of Escherichia coli acid phosphatase
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Dassa, J., Marck, C. and Boquet, P.L.
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156. .161
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133. .1
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188. .1486
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172. .177
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.138
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 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120
                                       ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA
                                                          ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60
                                                                                                                 Conservative
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1497. .152
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299. .301
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note="created by site directed mutagenesis"
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note="created by site direct
                                                                                                                                                                                                                                                                                                                                                               163. .1165
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note="created by site direct
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1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200		CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG		1148 TITATUGUCUGAKUACGATAACTAGUCUGGAAATCICGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACTGG	901 TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960 	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900	781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780 	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660 	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600 	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480	361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420 	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 360 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG 300 	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240	248 TTCCTCAACGAACGAACGCAACTGATAGGTCATCAGACGCATGGTCATCATGGT 307 121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	
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39840 ATGAAAGCGATCT	TGAA	Local Similarity 99.4%; les 1292; Conservative	Match 9	96_45 96_46 4600001 jon_(11_of_47)_of_U00	1 4 4 ·						96_19 1900001 96_20 2000001 96_21 2100001 96_22 2200001		96 12 1200001 96 12 1200001 96 13 1300001	•		ent Name 6_00 6_01 6_01	o on it into A.	1261 ATCGTGAATGAA 1448 ATCGTGAATGAA		
AGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 39899	CATTITIATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	Pred. No. 0; 0; Mismatches 8; Indels	Score 1287.8; DB 15; Length 110000;	001 4610000 001 4639675 100006 from base 1000001 (H00006 Escherichia coli K-12 MG1655	441000						001 2010000 001 2110000 001 2210000 001 2210000		-1111 -5432	101981	300001 410000 400001 510000 500001 510000 500001 610000	### ##################################	TOTIC TIONAL Property Tional	IGAAIGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300 		

241 GSACNTTACCAACGCCACGCTTTGCTAACGCCACGCATTTGCTGCCAAAAAAAGGCCTCCCCCCACGCATTTACCAACGCCACGCATTTTGCTACCACGCATTTGCTGCACGCAC	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTTAATTCTCATCGTTCATGGT 120
RESULT 13 APRODUCED 10 Sequence split into 47 fragments LOCUS APROSSA48 Accession APROSSA48 Fragment Name Begin End APROSSA48 On 100001 110000 APROSSA48 ON 100001 1100000 APROSSA48 ON 100001 11000000000000000000000000000	Db 40980 CAGATGCGTGATAAAACGCCGCGTGCATTAAATACGCCGGAGAGGTGAAACTGACC 41039 Qy 1201 CTGGCAGGATGTGAAAGAGCGAAATGCGCAGGGCATGTCGTTCGT

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Best Local Similarity
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AR636188.1
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Short, J.M., Kretz, K.A., Gray, K.A., Barton, N.R.,
O'Donoghue, E. and Mathur, E.J.
Recombinant bacterial phytases and uses thereof
Patent: US 685365-A 5 15-FEB-2005;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                               TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                                                                                                                                       GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG
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                                                                                                                                GCCTTCGCCGCGGGCTGGCACCTGACTGCCAATAACCGTACATACCCAGGCAGATACG
                                                                                                                                                                                                            CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA
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/mol_type="genomic DNA"
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from patent US 6855365.
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Sequence 9 :
AR636191
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      1 (bases 1 to 1901)
Short,J.M., Kretz,K.A., Gray,K.A., Barto
O'Donoghue,E. and Mathur,E.J.
O'Combinant bacterial phytases and uses
Patent: US 6855365-A 9 15-FEB-2005;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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Search completed: June 14, 2006, 14:10:08 Job time: 7402.95 secs

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Listing first 45 summaries
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Score
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Gapop 10.0 , Gapext 1.0
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10650.337 Million cell updates/sec
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1322
48236798 seqs, 27959665780 residues
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AW036132
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CA093060
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AA545747
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BUT13770 SJAABUG02
CF326092 JMT1--05-
CN752997 IDOAAA5DC
CN754382 IDOAAA1DP
BR520240 MILB12STM
AW036132 BST774510
BW713769 SJAABUG01
AA545747 HBMSF1B4-
CN759004 IDOAAA2BB
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AK168364 Mus muscu	AK146141 Mus muscu	BY737657 BY737657		AA521521 vi07b12.r	BB610221 BB610221		AI553154 vi07b12.y	CA566872 K0406H12-	BY056036 BY056036	BY041909 BY041909	BY053637 BY053637	BI152280 602917706	H60613 yr44d12.s1	CX943192 LamjGestG	DN201839 USDA-FP_1	CL665745 PRI014c_E		DX010757 KBrB001C0	CV672453 RET7SJ_01	CO386885 AGENCOURT	BE520241 M11B12XTM		BG457132 NF100C05P	BJ030203 BJ030203	BE461872 EST413291

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                     Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
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616 bp mRNA linear EST 29-SEP-2003
BJ074127 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL090j06 5', mRNA sequence.
BJ074127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus; Xenopus.
I (bases 1 to 616)
Itayama,A., Terasaka,C., Mochii,M., Ueno,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                 http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kohara,Y
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                     /tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
                                                                                                                                                                       /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL090j06"
                                                                                                                                                                                                                                                            1. .616
  46.5%;
99.8%;
  Score 614.4; DB 2;
Pred. No. 8.3e-180;
                      Length 616;
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RESULT 2
CL662734
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PRI0142b_B11 - I
pacificus var. (
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Evolutionary Biology
Max-Planck-Institute for Development
Spemannstr. 37-39, Tuebingen D-72076
Tel: 00497071601371
Pax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                       AppaDB: an AcedB database
Pristionchus pacificus
Nucleic Acids Res. 32 (1)
                                                                                                                                           Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                  survey sequence.
CL662734
CL662734.1 GI:5
                                                                   Contact: Sommer RJ
                                                                                                                       Srinivasan, J.,
                                                                               14681447
                                                                                                                                                                                                                                                                                                              CCGCGCCACCCCGTTA 879
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Class: fosmid ends.
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                   AGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                                GGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGC
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/mol_type="genomic DNA"
/strain="California"
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Pred. No. 4.3e-172;
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3', mRNA sequence.
CA093060
CA093060.1 GI:34946367
EST.
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Saccharum officinarum

officinarum

CA093060 SCCCCL2001D10.b CL2 3', mRNA sequence.

Saccharum

746 bp mRNA marum officinarum

linear EST 23-SEP-200: cDNA clone SCCCCL2001D10

EST 23-SEP-2003

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Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13/Forward primer.
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The libraries that made SUCEST
AACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAA
                                                                                                                                                                                                                                   CTACAACGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAG
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                                                                                                   GTACTGTTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTC
                                                                                                                                                   ACAGCGTTGACGCCCATCCACCGCANAAACAGGCGTATGGTGTGACATTACCCACTTCA
                                                                                                                                                                                          GCAGCGTTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCA
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/Clone | CL2"

/note="Organ: Pool of sugarcane calli submitted to low (4oC) and high (37 C) temperature stress; Vector: pslurScript; Site 1: EcoRI; Site 2: XhoI; An unidirectional cDNA library generated from [Pool of sugarcane calli submitted to low (4oC) and high (37 C) temperature stress]. cDNA was prepared from polyA+ mRNA using ZAP - cDNA Synthesis Kit (Stratagene). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm -columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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/db_xref="taxon:4547"
/clone="SCCCCL2001D10"
/lab_host="XL1Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Saccharum officinarum"
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Pred. No. 7.1e-153;
0; Mismatches 16;
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Schistosoma japonicum
Schistosoma japonicum
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 529)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
Evolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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SUAABUGO2 Adult SjC 7/94 Schistosoma japonicum cDNA similar to
pdb|1DKF|A Chain A, Crystal Structure Of Phytate Complex Of
Becherichia Coli Phytase At Ph 6.6. Phytate Is Bound With Its
3-Phosphate In The Active Site. Hg2+ Cation Acts As An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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Chinese National Huma
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BU713770
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                /tissue type="whole body"
//dev stage="Adult worms"
/lab_host="Mouse and rabbit"
/clone_lib="Adult SjC 7/94"
/clone_lib="Adult SjC 7/94"
/clone_lib="Adult SjC 7/94"
/clone_lib="Adult SjC 7/94"
/note="Wector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from Pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-XhoI-primer and synthesis was
primed with BCARI and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digsered with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Schistosoma japonicum"
/mol type="mRNA"
/strain="Chinese (Anhui) strain"
/db xref="taxon:6182"
/sex="Male and female"
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a small percentage, 2% to 3%,
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RESULT 5
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                                                                                      1 (bases 1 to 595)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T. Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Genomics and Genetics Institute, ( of Bioscience and Bioinformatics, Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                                                                                                                                               CP326092 595 bp mRNA linear EST 18-AUG-:
JWMI-05-B09.g1 AtJWT-overexpressing transgenic rice lambda phay
cDNA library (JWMI) Oryza sativa (japonica cultivar-group) cDNA
clone JWMI--05-B09, mRNA sequence.
                                                                       Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                       CF326092.1 GI:33800445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                         lade; Ehrhartoideae; Oryzeae; Oryza.
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nilarity 99.1%;
Conservative
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Pred. No. 1.2e-150;
); Mismatches 5;
                                             GreenGene Biotech Inc.;
                          MyongJi University
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lambda phage
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JOURNAL COMMENT

TITLE

REFERENCE AUTHORS

KEYWORDS

LOCUS

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KEYWORDS
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Best Local Similarity
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                                           CN762997
IDOAAA5DC09RM1 I
mRNA sequence.
CN762997
CN762997.1 GI:
EST.
Acyrthosiphon pisum
Acyrthosiphon pisum
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82 31 321 6355
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/clone="UMT1--05-B09"
/clone="UMT1--05-B09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
/clone_lib="AtJMT-overexpressing transgenic rice lambda
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; CDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                GI:47536920
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                                                                                             Acyrthosiphon
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                                                                                           pisum
                                                                                               CDNA
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WA clone IDOAAA5DC09 5',
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidodea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 895)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
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Contact: D. Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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TACGCCGCCGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGG 1232
                                                                         GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA 1172
                                                                                                                                                                 AGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA 1112
                                                                                                                                                                                                                                  TCTCGGCGGCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCC
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                                                                                                                                                                                                                                                                                                                             TEGTETEACATTACCCACTTCAGTECTETTTATCGCCGGACACGATACTAATCTGGCAAA
                                                                                                                                                                                                                                                                                                                                                               TGGTGTGACATTACCCACTTCAGTACTGTTTATTGCCGGACACGATACTAATCTGGCAAA 992
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                                           GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="ApMS" / clone lib="ApMS" / stee 1: EcoRI; Site 2: XhoI; note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: IDDAPA; Plant growth place: Department of Ecology & Evolutionary Blology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/199; Harvesting date: 01/06/199; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction: experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Acyrthosiphon pisum"
/mal_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
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98.6%;
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839 AACGCACGCCAGAGGTTGCCCGCAGCCCGCCACCCCGTTATTGGATTTGATCATGGCAG 898

Conservative

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Mismatches

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CN754382/c
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Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 868)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: CAGGAAACAGCTATGACC
Plate: 12 row: E column: 1.
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CN754382
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                                                                                             /clone_lib="ApMS"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_l: EcoRI; Site_2: XhoI;
/note="Vector: pBS-SK minus; Site_l: EcoRI; Site_2: XhoI;
/note="Vector: pBS-SK minus; Site_l: EcoRI; Site_2: Department of Bcology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XII-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="developmentstage"
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/clone="IDOAAA12DE01"
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/mol_type="mRNA"
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                     33.2%;
                     Score 438.8; DB 8; Pred. No. 6.1e-125;
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Acyrthosiphon pisum
Acyrthosiphon pisum
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hemiptera; Sternorrhyncha; Aphidiformes;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                   UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
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POlate: 1 row: F column: 9.
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CN757565.1 GI:47531488
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                                                                                                                                                                                                                     row: F column: 9. Location/Qualifiers
                                   tissue_type="whole insect"
/dev_stage="nymphs and adult
/lab_host="XL1-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus;
                                                                                                                       /cultivar="developmentstage"
/db_xref="taxon:7029"
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                                                                                                  clone="IDOAAA1DF09"
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CGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT 408

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Matches 450;
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CGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                                          GGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAAT 1262
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                                                                                                                                                                   GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACCCT
                                                                                                                                                                                               GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACCCT 1202
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                                                                   GGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAAT
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98.3%;
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BE520240/c
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                                                                                                                                JOURNAL
                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                    AUTHORS
                     11115976
Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                        1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE520240 393 bp mRNA linear M11B12STM Arabidopsis developing seed Arabidopsis
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BE520240
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224 Biochemistry, Michigan State University,
     East
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thaliana cDNA
     Lansing,
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REFERENCE
AUTHORS
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AW036132
LOCUS
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Best Local Similarity
Matches 388; Conser
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Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C.,
                                                           Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
                                                                                                                                                                                     EST.
                                                                                                                                                                                                    AW036132
383 bp mRNA linear EST 18-MAY-2001 EST274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036132
AW036132.1 GI:5894811
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Fax: 517 353 9334
Email: benning@mu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Bot
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTCATTAACCGGTGCGGTAAGCCTCGCATCA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTCAAGGTGAGCGCCGACAAT
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/note="Organ: Developing seed; Vector:
Site_1: EcoRI; Site_2: XhoII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coll"
/lab_nost="E.coll"
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/db_xref="taxon:3702"
/clone="M11B12"
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/mol_type="mRNA"
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Pred. No. 1.3e
0; Mismatches
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SOURCE ORGANISM

Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Solanaceae; Solanum; Lycopersicon.

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RESULT 11
AW036134/c
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VERSION
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DEFINITION
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Best Local Similarity
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             AW036134
383 bp mRNA linear EST 18-MAY-2001 EST274$10 tomato seed, TAMU Lycopersicon esculentum cDNA clone cLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036134
AW036134.1 GI:5894813
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Contact: CUGI
Clemson University Genomics Institute Clemson University
Clemson University Genomics Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.genome.clemson.edu/orders/index.html
3 prime sequence.
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ilarity 100.0%;
Conservative (
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/lab_host="XL1-Blue MRF'"
/clone_lib="tomato seed, TAMU"
/clore="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_Not; CLEE - Tomato Seed EST Library. Directionally clowns inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
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/clone="clee1823"
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/cultivar="TA496"
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Pred. No. 1.3e-107;
0; Mismatches 0;
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                                                                   BU713769
SJAABUGOI Adult SjC 7/94 Schistosoma japonicum cDNA similar to sp[p07102|ppA_ECOLI_PERIPLASMIC APPA_PROTEIN PRECURSOR [INCLUDES: PHOSPHOANHYDRIDE PHOSPHOHYDROLASE (PH 2.5 ACID PHOSPHATASE) (AP);
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BU713769.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fordan Hall, Clemson, SC 29634, USA
i: http://www.genome.clemson.edu/orders/index.html
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/lab_host="XL1-Blue MRF'"
/clone lib="tomatc seed, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site
/note="Vector: pBlueScript SK(-) at 5' end with
EcoR1 and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="seeds"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Lycopersicon
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; Pred. No. 1.3e-107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBMED
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670 GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT 729
                                                                                    425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schistosoma japonicum
Schistosoma japonicum
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                                                                                                             Similarity
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86-21-50801922
                                                                                                                                                                                                                                                 /tissue type="male and remain ()
/tissue type="whole body"
/lab_host="whole body"
/lab_host="whole body"
/clone lib="Adult SjC 7/94"
/clone lib="Adult SjC 7/94"
/clone lib="Adult SjC 7/94"
/clone lib="Adult SjC 7/94"
/khol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (GJMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
GIMR from lysates of these worms by oligo dT
chromatography, using a kit from Pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-Xhol-primer and synthesis was
primed with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to Rocal linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
clones contain inserts that appear to be highly homologous
to sequences from salmonoid fishes, as determined by
homology comparisons using BLAST and by Southern
hybridization analysis to genomic DNA from salmon (Sigma
chemical Co., St. Louis, MO) under stringent washing
conditions. The remainder of the clones appear to contain
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hanzg@chgc.sh.cn
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/strain="Chinese (Anhui)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Schistosoma"
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                                                                                                                                                                                                                              japonicum sequences."
                                                                                                             26.4%;
                                                                                                             Score 348.6; DB 3
Pred. No. 7.9e-97;
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RESULT 13
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AUTHORS
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clone HEMSF1B4 5', mRNA 8
AA545747
AA545747.1 GI:2307026
EST.
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                                                                                                                                                                                                                                                                                                                  Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda,
Tel: 301-402-4877
Pax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                         Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Marra, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., Wylie, T., Waterston, R., Wilson, R. and Francomano, C. Washu, MGB/NHGRI EST Project
                                                                                                                                                                                                                                                                                                      Fax: 301-496-7157
Email: libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Libin Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
1 (bases 1 to 354)
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                                                                                                                                                                                                                                                                      primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482
                                                                                               /sex="Male and Female"
/tissue_type="bone marrow"
/cell_type="stromal fibroblast"
/dev_stage="mixed"
/lab_host="%%1-Blue"
                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMSF1B4"
                                                                 /clone_lib="Hu
/note="Vector:
                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
 23.0%;
94.9%;
                                                            lib="Human Bone Marrow Stromal Fibroblast"
"Vector: pBluescript, Site_1: EcoRI; Site_2
Score 304.6; DB 1; Pred. No. 3.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 bp mRNA linear EST 12-MAY-1999
Marrow Stromal Fibroblast Homo sapiens cDNA
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                                                               Site_2:
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ACCESSION
VERSION
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DEFINITION
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CN759004/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acyrthosiphon pisum

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 706)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Muster, D., Tagu, D. and Mincker, P.

Stern, D., Tagu, D. and Mincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                          Risk of contamination by bacterial sequences from obligatory (Buchhera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR PRImers
                                                                                                                                                                                                                                                                                                                                                                                                                           UMR B103P, BP 35327, F
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: D. Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN759004 706 bp mRNA IDOAAA24BCO4RM1 ApmS Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                      Plate: 24 row:
                                                                                                                                                                                                                                                                                        FORWARD: CAGGAAACAGCTATGACC
Plate: 24 row: C column: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An expressed sequence tags database for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acyrthosiphon pisum (pea aphid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTCTCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGAACTGGAACGGGTG-TTAATTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: IDOAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999;
                                                          /clone_lib="ApMS"
/note="Vector:_pB
                                                                                              /clone="IDOAAA24BC04"
/tlssue_type="whole insect"
/dev_stage="nymphs and adults
/lab_host="XL1-Blue"
                                                                                                                                                                                        organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                            db_xref="taxon:7029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F-35653 Le Rheu Cedex France
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DNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pea aphid Acyrthosiphon
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Aphidiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 20-MAY-2
ID0AAA24BC04
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KEYWORDS
SOURCE
ORGANISM
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BJ619443
LOCUS
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VERSION
ORIGIN
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Best Local Similarity
Matches 297; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                              Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ619443

TO7 bp mRNA linear EST 01-OCT BJ619443 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL189d24 5', mRNA sequence.
                                                                                                                                                                                                                                                                               Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ619443
BJ619443.1 GI:37258203
                                                                                                                                                                                                                                      http://xenopus.nibb.ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTTGAGAT 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All partheonemente stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                   /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XI189d24"
                                        /tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized
                                                                                                                                                                                                           nopus.nibb.ac.jp.
location/Qualifiers
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                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                 available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 8;
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                                           Xenopus
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                                        gastrula
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Best Local :
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                                                                                                                                                                                                                                                                     251;
241
                        990
                                                                             930
                                                                                                        121
                                                                                                                                   870
                                                                                                                                                                                         810
                                                                                                                                                                                                                                            750 AATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAACACCTTGCTAAG
                                                                                                                                                              61
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                                                                     GTATGGTGTGACATTACCCACTTCAGTACTGTTTATTGCCGGACACGATACTAATCTGGC 989
AAATCTCGGCGGCGCA
                     AAATCTCGGCGGCGCA 1005
                                                    GTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGC
                                                                                                                                CACCCCGTTATTGGATTTGATCATGGCAGCGTTGACGCCCCATCCACCGCAAAAAACAGGC
                                                                                                                                                                                         TTTGCATAACGCGCAATTTTATTTGCTACAACGCACGCCAGAGGTTGCCCGCAGCCGCGC
                                                                                                                                                                                                                  ANTGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAACACCTTGCTAAG
                                                                                                        CACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAGGC
                                                                                                                                                              TTTGCATAACGCGCAATTTTATTTGCTACAACGCACGCCAGAGGTTGCCCCGCAGCCGCGC 120
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                   18.8%;
256
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                     Score 248; DB 2;
Pred. No. 2.2e-65;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                Length 707;
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                                                                                                          180
                                                     240
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Search completed: June 14, 2006, 14:21:54 Job time : 6948.38 secs

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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence:
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                                                                                                                                                                                                                                                               Score
 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                       87554321
                                                                                                                                                                                                                                                              Match
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290227 seqs, 117694381 residues
                                                                                                                                                                                                                                                                                                                                                   1 atgaaagcgatcttaatccc.....atcaccatcaccatcactaa 1323
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 Copyright
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GenCore version (c) 1993 - 2006
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       US-10-449-902-20908
US-11-293-6597-2180
US-10-953-349-31004
US-11-217-529-79920
US-11-217-529-79920
US-11-217-529-79920
US-10-449-902-13863
US-10-449-902-12516
US-10-449-902-12516
US-10-449-902-12516
US-10-449-902-15013
                                                                                                                                                                                                                                                                                            SUMMARIES
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Biocceleration Ltd
               Sequence 20908, A
Sequence 2180, Ap
Sequence 34412, Ap
Sequence 11004, A
Sequence 9997, App)
Sequence 6188, Ap
Sequence 17204, A
Sequence 17266, A
Sequence 10760, Ap
Sequence 10760, Ap
Sequence 10760, Ap
Sequence 11476, A
Sequence 11476, A
Sequence 22962, App
Sequence 22962, App
Sequence 22962, App
Sequence 13013, A
Sequence 13013, A
Sequence 80383, A
Sequence 80383, A
Sequence 80383, A
Sequence 80383, A
       sequence
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26 29.4 2.2 718 7 US 28 29.4 2.2 956 6 US 28 29.4 2.2 956 6 US 29 29.4 2.2 1161 7 US 31 29.4 2.2 2071 6 US 31 29.4 2.2 2754 7 US 32 29.4 2.2 2754 7 US 33 29.2 2.2 1627 6 US 34 29.2 2.2 1627 6 US 35 29.2 2.2 1627 7 US 36 29 2.2 3158 6 US 37 28.8 2.2 3457 7 US 38 28.8 2.2 3457 7 US 39 28.8 2.2 31544 7 US 41 28.6 2.2 1105 6 US 41 28.6 2.2 1105 6 US 42 28.6 2.2 1106 6 US 43 28.6 2.2 1108 6 US 44 28.6 2.2 1108 6 US 45 28.4 2.1 1445 6 US	26 29.4 2.2 71.8 7 US 28 29.4 2.2 71.8 7 US 28 29.4 2.2 807 7 US 29 29.4 2.2 1161 7 US 31 29.4 2.2 2071 6 US 31 29.4 2.2 2754 7 US 32 29.4 2.2 2754 7 US 33 29.2 2.2 1627 6 US 34 29.2 2.3 168 6 US 35 29 2.2 3168 6 US 36 29 2.2 3457 7 US 37 28.8 2.2 3457 7 US 38 28.8 2.2 3457 7 US 39 28.8 2.2 11544 7 US 40 28.6 2.2 1152 6 US 41 28.6 2.2 1312 6 US 41 28.6 2.2 1312 6 US 42 28.6 2.2 1808 6 US 44 28.6 2.2 1808 6 US 45 28.4 2.1 1445 6 US
29.4 2.2 718 7 US 29.4 2.2 807 7 US 29.4 2.2 807 7 US 29.4 2.2 956 6 US 29.4 2.2 2071 6 US 29.4 2.2 2072 6 US 29.4 2.2 2754 7 US 29.2 2.2 772 6 US 29.2 2.2 3168 6 US 29.2 3168 6 US 29.2 3164 7 US 29.8 2.2 3457 7 US 28.8 2.2 3457 7 US 28.6 2.2 1105 6 US 28.6 2.2 1105 6 US 28.6 2.2 11881 6 US 28.6 2.2 11881 6 US 28.4 2.1 1445 6 US	29.4 2.2 702 6 US-10-449-902-5189 Sequence 518 29.4 2.2 708 7 US-11-154-977-68 Sequence 62, 29.4 2.2 807 7 US-11-154-977-42 Sequence 62, 29.4 2.2 956 6 US-10-449-902-11182 Sequence 36, 29.4 2.2 1956 6 US-10-449-902-11182 Sequence 36, 29.4 2.2 2071 6 US-11-154-977-36 Sequence 36, 29.4 2.2 2071 6 US-11-217-529-5697 Sequence 569 29.4 2.2 2754 7 US-11-217-529-5697 Sequence 569 29.2 27.7 6 US-10-449-902-18030 Sequence 180 29.2 27.7 6 US-10-449-902-18030 Sequence 180 29.2 2.1 627 6 US-10-449-902-12853 Sequence 128 29.2 2.2 3168 6 US-10-449-902-25001 Sequence 250 28.8 2.2 3158 6 US-10-449-902-25001 Sequence 248 28.8 2.2 31544 7 US-11-293-697-1224 Sequence 12, 28.6 2.2 11544 7 US-11-293-697-1224 Sequence 12, 28.6 2.2 11544 7 US-11-246-405-12 Sequence 741 28.6 2.2 1312 6 US-10-449-902-76896 Sequence 741 28.6 2.2 1312 6 US-10-449-902-2555 Sequence 255 28.6 2.2 1808 6 US-10-449-902-2555 Sequence 255 28.6 2.2 1808 6 US-10-449-902-2555 Sequence 255 28.6 2.2 1808 6 US-10-449-902-2555 Sequence 255 28.6 2.2 1445 6 US-10-449-902-2555 Sequence 255 28.6 2.2 1445 6 US-10-449-902-2555 Sequence 251
2.2 7102 6 US 2.2 807 7 US 2.2 807 7 US 2.2 956 6 US 2.2 2071 6 US 2.2 2754 7 US 2.2 172 6 US 2.2 3168 6 US 2.2 349 6 US 2.2 3457 7 US 2.2 11544 7 US	2.2 702 6 US-10-449-902-5189 Sequence 518 2.2 708 7 US-11-154-977-68 2.2 807 7 US-11-154-977-68 2.2 807 7 US-11-154-977-42 Sequence 42, 2.2 956 6 US-10-449-902-11182 Sequence 36, 2.2 2071 6 US-10-449-902-24250 Sequence 36, 2.2 2071 6 US-11-217-529-5697 Sequence 569 2.2 2754 7 US-11-217-529-5697 Sequence 569 2.2 2754 7 US-11-249-902-18030 Sequence 697 2.2 1627 6 US-10-449-902-12853 Sequence 697 2.2 1627 6 US-10-449-902-25001 Sequence 128 2.2 3458 6 US-10-449-902-25001 Sequence 248 2.2 3457 7 US-11-246-405-12 Sequence 12, 2.3 11544 7 US-11-246-405-12 Sequence 12, 2.3 11544 7 US-11-246-405-12 Sequence 741 2.2 11005 6 US-10-449-902-24867 Sequence 741 2.2 11203 7 US-11-249-902-8467 Sequence 255 2.2 1808 6 US-10-449-902-25550 Sequence 255 2.1 1445 6 US-10-449-902-25655 Sequence 255 2.1 1445 6 US-10-449-902-25655 Sequence 251
	.2 702 6 US-10-449-902-5189 Sequence 518 .2 718 7 US-11-154-977-62 .2 807 7 US-11-154-977-62 .2 956 6 US-10-449-902-11182 Sequence 42, .2 1161 7 US-11-154-977-36 .2 1161 7 US-11-154-977-36 .2 12754 7 US-11-217-529-5697 Sequence 242 .2 2774 7 US-11-217-529-5697 Sequence 569 .2 1772 6 US-10-449-902-18030 Sequence 697 .2 1627 6 US-10-449-902-12853 Sequence 697 .2 3168 6 US-10-449-902-25001 Sequence 128 .2 3457 7 US-11-249-902-25001 Sequence 128 .2 3457 7 US-11-249-902-274808 Sequence 128 .2 3457 7 US-11-246-405-12 Sequence 128 .2 3457 7 US-11-239-76896 Sequence 128 .2 11544 7 US-11-246-405-12 Sequence 128 .2 1154 7 US-11-246-405-12 Sequence 258 .2 1154 0 US-10-449-902-8467 Sequence 268 .2 1312 6 US-10-449-902-25550 Sequence 268 .2 1312 6 US-10-449-902-25550 Sequence 268 .2 1316 6 US-10-449-902-25550 Sequence 275 .1 1445 6 US-10-449-902-21495 Sequence 251
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800 800 800 800 800 800 800 800 800 800	US-10-449-902-5189 US-11-154-977-68 US-11-154-977-68 US-11-154-977-42 US-10-449-902-11182 US-10-449-902-11182 US-10-449-902-24250 US-10-449-902-12853 US-10-449-902-2550 US-11-246-405-12 US-11-246-405-13 US-11-2
US-10-449-902-5189 US-11-154-977-68 US-11-154-977-42 US-10-449-902-11182 US-11-449-902-1285 US-11-449-902-18030 US-11-217-529-5697 US-11-449-902-18633 US-11-449-902-25001 US-10-449-902-274808 US-11-233-697-1224 US-11-233-697-1224 US-11-246-405-12 US-11-246-405-12 US-11-247-529-76896 US-10-449-902-25550	-10-449-902-5189 Sequence 518 -11-154-977-68 Sequence 68, -11-154-977-42 Sequence 68, -11-154-977-42 Sequence 61, -11-154-977-35 Sequence 21, -11-154-977-35 Sequence 21, -11-154-977-35 Sequence 24, -11-154-977-35 Sequence 24, -11-217-529-567 Sequence 120, -10-449-902-18030 Sequence 120, -10-449-902-24808 Sequence 120, -10-449-902-24808 Sequence 120, -10-449-902-24808 Sequence 121, -11-217-529-6896 Sequence 12, -10-449-902-8467 Sequence 768, -10-449-902-8467 Sequence 255, -10-449-902-25550 Sequence 255, -10-449-902-25555 Sequence 255, -10-449-902-25555 Sequence 255, -10-449-902-25555 Sequence 255, -10-449-902-25555 Sequence 255,
	518 428, 1111 2569 1699 1742, 1248 1744, 1

ALIGNMENTS

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Sequence 20008, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-0A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: JD 2002-203269
PRIOR APPLICATION NUMBER: JD 2002-383870
PRIOR APPLICATION NUMBER: JD 2002-383870
PRIOR APPLICATION DATE: 2002-12-11
NUMBER: DF SEQ ID NOS: 56791
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US-10-449-902-20908/c
                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20908
LENGTH: 1309
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: OTYZA SATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK071209
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                  Local Similarity
591
                                         332
                                                                                                                                     272
                                                                                                                                                                                                                              212
                                                                                                                                                                                                                                                                              96;
                               TCGACGAGCGTACCCGTAAAACAGGCGAAGCCTTCGCCGCCGCGGCTG
ACGAGGCGCATGTCGTGCGACTCGGCGCTGCCGTCGACGGCGAGCGG
                                                                                       ACGAACTCCTGGAGGACGAGGCGCGCGCGCGGAGGAGGGACGCCCGTCGCGGCGGTAG
                                                                                                                                acegarieciegecaaaaaaeeeciecececaeiciecaeicaecicecariatiecieare
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                                                                                                                                                                                                                                                                          2.9%;
nilarity 51.5%;
Conservative
                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                          Score 38; DB 6; Length 1309; Pred. No. 0.0051; O; Mismatches 81; Indels
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RESULT 2 US-11-293-697-2180/c ; Sequence 2180, Application US/11293697

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; Publication No. US20060105376A1
; GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOWel full length cDNA
FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR PILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
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; SEQ ID NO 2180
; LENGTH: 2879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2180
밁
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                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34412
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.2
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.3
SEQ ID NO 34412
LENGTH: 979
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579 PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                              649
529
                                    343
                                                                       589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 AACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTCGGACATTACCAAC
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                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                  GCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATGGTGTGGCGGAAGTCGCCCAGCGGGGGCGCTGATCATCTCGGCCGTGAGGTCCGCTC
GTCGGTGAGAGAGGCG 514
                                    ACCCGTAAAACAGGCG 358
                                                                         GCGGGCGAGGCAGTCGCGGGACCGCGTGCACGACCGGTAGAGGCTGAGCACGGCGAGCCA 530
                                                                                                                                                GAGCCGATCGACGAGACGGGCCTTCGCCGGCGGCGGAGCGCGGGGGCGCAGCGGCGT 590
                                                                                                                                                                                   GAGCTAATCGCCTATCTCGGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTG
                                                                                                                                                                                                                        ACACCCGGCGAAGGACCGGGAGCACCGGGACACGCGGACCTGGCTCACTGGTGAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCGGCCTTGCTATTGAGGAAGGAGGTGTCCCCCAAAGGCGTCTCCGGCCCGGCCCAACGT
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US-10-953-349-11004/c
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
CORTENANT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 79920
LENGTH: 1257
TYPE: NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 11004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79920, Application US/11217529 Publication No. US20060099612A1
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                                                                                                                                                                           Matches
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                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKANURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2271
TYPE: DNA
                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                 ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.5%;
Local Similarity 60.4%;
                                                                                                                                                                         Local Similarity
nes 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1734 TGAACCGGGACATGTTCGGGTGATATGTACCTGAGAAGGGTTTCTGCAGATCTTGAAGGA 1675
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                                                                                                                              671 CCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTC 730
193
                                        731 TCCTGCAACAAGCACAGG 748
                                                                                   CCGAGTCTGTCTCAAAAATGGGTTTGGTGAGCGTGCCATCAGCGCTGAAGGAGCCGTATT
  TCATCCAATCCGTAGAGG
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                                                                                                                                                                                       2.5%;
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  176
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                                                                                                                                                                                                                  DB 7;
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                                                                                                                                                                                                                  Length 1257;
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RESULT 6 US-11-293-654-37

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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Poundation for Advancement of International Science.
ITITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 8987
LENGTH: 1396
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APPLICANT: Taraporewala, Zenobia F.

TITLE OF INVENTION: ANTIGEN DELIVERY PLATFORM

FILE REFERENCE: 4239-99406-02

CURRENT APPLICATION NUMBER: US/11/293,654

CURRENT FILING DATE: 2005-12-02

PRIOR APPLICATION NUMBER: US 60/633,036

PRIOR FILING DATE: 2004-12-03

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.3

SEQ ID NO 37

LENGTH: 3431
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Best Local Similarity
Matches 46; Conserv
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Publication No. US20060123505A1
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Publication No. US20060122368A1
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK106335
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                 10-449-902-8987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Vector
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                                                                                                           Local
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                                          679 GTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTCTCCTGCAA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 ACAGAATTCATTAAAGAGGAGAAATTAACCATGGGAGGATCCAGATCTCATCACCATCAC 144
                                                                                                             Similarity
GTCTCGTTCTCGGTCGCGGTCGCCTTCTCGCCGAAGCGGGAGGAGCTCGTACTCCGAGAA
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                                                                                                           Score 32;
Pred. No.
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Pred. No. 1;
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                                                                                                           DB 6; Length 1396; 0.68;
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                                                                                    Gaps
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515
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GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

ITITE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791
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                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 17204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17204, Application US/10449902 Publication No. US20060123505A1
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Publication No. US20060123505A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK104957
DATABASE ENTRY DATE: 2002-08-28
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APPLICANT: Bio-oriented Technology Research Advancement Institut
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 2002-203269 PRIOR FILING DATE: 2002-05-30
ORGANISM: Oryza sativa
                                                ENGTH: 1600
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les 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 CGACGAGCGTACCCG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 CGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTATTGCTGATGT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 GCGNGGTGGTGAGCTAATCGCCTATCTCGGACATTACCAACGCCAGCGTCTGGTAGCCGA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 CCGGCATGGGACAGGCGCGCGACGATGGTGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCGAGCACCTTCTCCAGCTCGGCGCTCACCACCATCAGGTCGTCCTCCGTGGTGGTGT
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US-10-449-902-13863/c
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RESULT 11
US-10-449-902-12516/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-449-902-13863
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SEQ ID NO 13863
LENGTH: 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13863, Application US/10449902 Publication No. US20060123505A1
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Bio-oriented Technology Research Advancement Institut
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: T002-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK067664
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK111211
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2002-383870 PRIOR FILING DATE: 2002-12-11 NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                   2762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495
                                                                                                                                                                                                                                                                                                                                                                                  999 CGGCGCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 CGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTATTGCTGATGT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 GCGGGCAGTCGACGCCACCGCCATGGCGAAGCTCACCCCGCGCCGACGCCACGTCGACGC 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 GCGNGGTGGTGAGCTAATCGCCTATCTCGGACATTACCAACGCCAGCGTCTGGTAGCCGA 272
                                                                                                                                                                                                                                                                                                                                                                                                                            92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACGAGCGTACCCG 347
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                                                                                   ACCAGGAGTGCTG 2750
                                                                                                                            GCCCGGAGAGGTG 1191
                                                                                                                                                                      GGTGAACCCGGAGATGTTGGAGAGCATGGAGGAGGAACGGCCGCGCCATTGCGGAGGGA 2763
                                                                                                                                                                                                   GCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCC
                                                                                                                                                                                                                                                       TGCGTGGAACGGGTTACCGAGTTGGAAGCCAGAGGGTGAGTGCGGCTCGTCGAAGCCATC
                                                                                                                                                                                                                                                                                               TGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTC
                                                                                                                                                                                                                                                                                                                                        CGAAGTTCCGGAGCTCAGACTGCCGCTGCCATGGCTTCCGTTGCGCCCGTTGAGATGGGG
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; Pred. No. 1;
0; Mismatches
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Pred. No. 1.8;
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US-10-449-902-10760
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                                                                                                                                   SEQ ID NO 10760
LENGTH: 1344
TYPE: DNA
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Publication No. US20060123505A1
GENERAL INFORMATION:
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Publication No. US20060123505A1
GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 2144
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: FOUNDATION OF ADVANCEMENT OF INTERIOR SCIENCE.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UF 10/449,902
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
NUMBER OF SEQ ID NOS: 56791
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Dyssical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A9205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                       ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108108
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: OTYZA BATİVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK109864
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1532 GTCCACCCACGTCTCGTTGTTGCCGGAGCCGCCGGCGGCGGCGGCGGCGTCCCAGC 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1592 GTTGTAGTGGTTCGCCGCGATCGCCACCTTCTTCTTCCTCAGCTTCCGCCTTGCGGACGAA 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1652 CGGCGGGGTGGGCAGCCAGCTGGCTCAGCCGGAGGTACTCCATCCCCTTCTTCTCGTCGCG 1593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTATTGCTGAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 1.7;
0; Mismatches
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Query Match

Best Local Similarity

2.3%;

Score 31; Pred. No.

DB 1.5;

6

Length 1344;

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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NOVel full length cDNA; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 707
; LENGTH: 2791
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                                                                                                                                                                                                                   ; ORGANISM: Triticum aestivum US-10-953-349-27515
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; ORGANISM: Homo sapiens
US-11-293-697-707
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US-11-293-697-707/c
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27515
LENGTH: 1393
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27515, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                           TYPE: DNA
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663 GGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 GATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAAGCCTTCGCCGCCGGGC 376
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                                                          TAACCTTTAGGTÁCATCTTGCÁGGTTCTACCAACÁGGTÁAGCTTAACAGCTGACAGTCCÁ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAG 169
                                                                                              ТАЛАССТСЯGАЛАСАССВАССВАЛАССТСТТСАТТАЛСССЛЕССАТТАССАТСССВАЛСТСЛА 662
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                                                                                                                                          Conservative
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Conservative
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Search completed: June 14, Job time: 41.2281 secs
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SEQ ID NO 11476
LENGTH: 1461
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108824
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-866-379-7

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US-09-866-379-5

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US-10-430-356-1

US-10-601-319-1
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Sequence 1, Appli
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12.4	12.4	12.4	12.4	15.1	15.6	16.3	16.6	16.9	29.5	29.5	30.2	30.2	50.4	50.4	52.1	55.1	94.7	94.7	94.9	95.5	95.6	95.6	95.7	95.7	95.7	97.0	97.0
254	254	254	254	356	1326	1325	1325	1326	1264	1264	466	4050	1281	1281	1737	11357	1486	1486	1296	1486	1489	1489	1308	1308	1308	1901	1901
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ALIGNMENTS

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ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1320)
NAME/KEY: misc feature
LOCATION: (1)..(1323)
OTHER INFORMATION: n is any nucleotide
US-09-777-566A-1
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/777,566A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
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US-09-777-566A-1
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
FILE REFERENCE: DIVER1370-6
Query Match
Best Local Similarity
Matches 1323; Conserv
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1323
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GENERAL INFORMATION:
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100.0%; Score 1322; Conservative 0; Mismatches
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OTHER INFORMATION:

US-09-866-379-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BARLEY, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT APPLICATION NUMBER: US/09/860,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/290,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF 520 ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1323
TYPR: DNA
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Sequence 1, Application US/10034985
Publication No. US20030049815A1
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION: NUMBER: US/10/034,985
CURRENT PILING DATE: 2001-12-21
PRIOR PELICATION NUMBER: US/9/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,798
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR PILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ROANISM: Escherichia coli
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Best Local Similarity 100.0%; F
Matches 1323; Conservative 0;
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NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C o)
                          GCCTTCGCCGCGCGCGCACCACCACGACTATAACCGTACATACCCCAGGCAGATACG
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GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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Pred. No. 0;
0; Mismatches
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RESULT 4
US-10-430-356-1
US-10-430-356-1
; Sequence 1, Application US/10430356
; Publication No. US20030232041A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
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CURRENT APPLICATION NUMBER: US/10/430,356
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
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Best Local
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LOCATION: (1)...(1323)
OTHER INFORMATION: n =
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NAME/KEY: CDS
LOCATION: (1)...(1320)
FEATURE:
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ORGANISM: Escherichia
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Similarity 100.0%;
23; Conservative 0
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                                      CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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Sequence 1, Application US/10601319
Publication No. US20040091968A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Short, Jay M.
APPLICANT: Short, Jay M.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, Nelson Robert
APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: ARCOMBINANT PHYTASES AND
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-059011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/866,379
PRIOR APPLICATION NUMBER: US/9/866,379
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US-10-601-319-1
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PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PRILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
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Best Local Similarity 100.0%;
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                                                                          CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PH
TITLE OF INVENTION: NUMBER: US/10/933,115
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT PILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
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PRIOR APPLICATION NUMBER: US 09/291,931
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Publication No. US20050281792A1
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PRIOR APPLICATION NUMBER: US 08/910,79
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1323
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Matches 1323;
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PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 1909-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 7
LENGTH: 1901
TYPE: DNA
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US-09-866-379-7
; Sequence 7, Application US/09866379
; Patent No. US20020136754A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                           APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KEETZ, Keith
APPLICANT: BARTON, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT PILING DATE: 2001-05-24
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1).-(1901)
; OTHER INFORMATION: n is any nu
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Query Match 97.4%; Score 1287.8; DB 6; Length 1901; Best Local Similarity 99.5%; Pred. No. 0;	; NAME/KEY: misc reature ; LOCATION: 403 - ; OTHER INFORMATION: n = A,T,C or G US-10-156-660-3	FEATURE: NAME/KEY: LOCATION: FEATURE:	3 1901 A : Escherichia coli	PRIOR PRIOR NUMBER SOFTWA		PRIOR PRIOR PRIOR PRIOR	CURREN CURREN PRIOR PRIOR	APPLICANT: Mathur, Eri- TITLE OF INVENTION: PHY TITLE OF INVENTION: AND FILE REFERENCE: 09010-0:		Publication GENERAL INFO APPLICANT: APPLICANT:		Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	Qy 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAGAGGTGAAACTGACC 1200	Qy 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	Qy 961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020	
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1021 AUGUTTU COGTICAGU COGATANCA COCUCAGOT GO TOMACUT GOTOT TOMACO TOG 				781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG	601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG	361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGGTGAGCTAATCGCCTATCTC	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT	1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA	MACCHER 1293; COMBETACTIVE 0; MIRWACCHER 1; INDEIR 0;

Query Match Query Match Best Local Similarity 99.5%; Pred. No. 0; Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Qy 1 ATGANAGCGATCTTAATCCCATTTTTATCTCTTGATTCCGTTAACCCCGCAATCTGCA 60	<pre>, NAME/KEY: CDS ; LOCATION: (188)(1483) ; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: 403 ; OTHER INFORMATION: n = A,T,C or G US-10-601-319-7</pre>	997-08 10 C Wind	PRIOR FILING DATE: 2000-05-25 PRIOR APPLICATION NUMBER: US 09/318,528 PRIOR FILING DATE: 1999-05-25 PRIOR APPLICATION NUMBER: US 09/291,931 PRIOR FILING DATE: 1999-04-13 PRIOR PILING DATE: 1999-04-13 PRIOR FILING DATE: 1999-03-01 PRIOR FILING DATE: 1999-03-01 PRIOR PILING DATE: 1999-03-01	; FILE REFERENCE: 09010-039011 ; CURRENT APPLICATION NUMBER: US/10/601,319 ; CURRENT FILING DATE: 2003-06-20 ; PRIOR APPLICATION NUMBER: US 09/866,379 ; PRIOR FILING DATE: 2001-05-24 ; PRIOR FILING DATE: US 09/580,515	APPLICANT: Gray, Kevin A. APPLICANT: Barton, Nelson Robert APPLICANT: Garrett, James B. APPLICANT: O' Donoghue, Eileen APPLICANT: Mathur, Eric J. TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING TITLE OF INVENTION: AND USING THEM	RESULT 9 US-10-601-319-7 ; Sequence 7, Application US/10601319 ; Publication No. US20040091968A1 ; GENERAL INFORMATION: ; APPLICANT: Kretz. Keith A.	Qy 1261 ATCGTGAATGAAGGACGCATACCGGCGTGCAGTTTGAGAT 1300	Db 1328 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCCCGGGAGGGTGAAACTGACC 1387 Oy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTGGCAGGTTTTACGCAA 1260	Qy 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140
8 8 8 8 8	B & B ;	S B S B 4	ב אל אל ליל ליל ליל ליל ליל ליל ליל ליל ל	S B S	D Q D Q	B Q B Q	QV dd	95 QV DB	& & &
1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGATGAACTGGTGTTTGAACGCTGG 1080		901 TTGACGCCCAGCGCAAAAAAAAAAACGGCGTTATGCGTTGACGTGTTAACGCCAATTTTAATCAGGAAATAGGCGCAATTTTGATCAGGAAACACGCGCAAAACACGCGCAATTTTAATTTGCTACAAA 1027 841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCACCCCCGTTATTGGATTTGATCATGGCAGCG 900	AAGGTGAGCCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACCGGAGATATTTCTCCCTGCAACAAGCACACGGGAATGCCGGAGCCGGAGCCGGGGGGGAAGGATCACCCCCCCC	CTTANACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	361 GCCTTCGCCGCCGGCTTGCCACCTGACTGTGCAATAACCCTACATACCCAGGCAGATAACG 420	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGGCGTACCCGTAAAACAGGCGAA 360	368 ACCTGGCCGGTAAAACTGGGTTGGCTGACCACCGCGNGGTGGTGAGCTAATCGCCTATCTC 427 241 GGACATTACCAACGCCAGCGTCTGGTAGCCACGACGGACTGCCCG 300	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180

ATGANAGCGATCTTAATCCCATTTTTATCTCTGATTCCGGTAATCCCCGCAATCTGCA 60	S-1 Qu Be	> - 1	PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER SOPTWA	CURRENT APPLICATION NUMBER: US/10/933,115 CURRENT FILING DATE: 2004-09-01 PRIOR APPLICATION NUMBER: US/09/866,379 PRIOR FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 09/580,515 PRIOR APPLICATION NUMBER: US 09/318,528 PRIOR APPLICATION NUMBER: US 09/318,528	Gray, Kevin A Barton, Nelso Bartot, Jame O' Donoghue, Mathur, Eric NVENTION: RECOM NVENTION: THER	RESULT 10 US-10-933-115-7 ; Sequence 7, Application US/10933115 ; Publication No. US20050281792A1 ; GENERAL INFORMATION: ; APPLICANT: Short, Jay M. ; APPLICANT: Kretz, Keith A.	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTTACGCAA 1260
5 6 6 6 6 6) B Q B Q	04 04 05	0 QV QV	B & B &	D	B & B &	0 Qy
126 CTGGCGATAACGATACAGCCTGTGATTTCAGTTTCGTTGGCAGATTTACAGATTTCAGATTTCAGTTTTCCAGATTTACAGATTTACAGATTTCAGTTTTCCAGATTTACAGATTACAGATTACAGAATATACAGAATTACAGAATATACAGAATATACAGAATATACAGAATATACAGAATATACAGAATATACAGAATATACAAATAAAT	TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGCACCG 900	721 GAGATATTTCTCCTGCAACCAGCGAATGCCGGAGCCGGGGAGCGGGGAGGATCACC 780		481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	361 GCCTTCGCCGGCCGGGCTGGCACTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG 300

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Sequence 3, Application US/11056354
Publication No. US20050246780A1
GENERAL INFORMATION:
APPLICANT: SHORT, Jay M.
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevith A.
APPLICANT: GRAY, Kevith A.
APPLICANT: GRAY, Kevith A.
APPLICANT: GARRETT, James B.
APPLICANT: GARRETT, James B.
APPLICANT: GARRETT, James B.
APPLICANT: O'DONOGHUS, Eileen
APPLICANT: O'DONOGHUS, Eileen
APPLICANT: HATHUR, Eric J.
TITLE OF INVENTION: PROR MAKING AND USING THEM
FILE REFERENCE: 564462001803/D1370-9C1
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/590
PRIOR APPLICATION
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; TYGANISM: E8cherichia coli appA phytase
; CRGANISM: E8cherichia coli appA phytase
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (403)...(403)
; OTHER INFORMATION: n is any nucleotide
US-11-056-354-3
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; Sequence 7167, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
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APPLICANT: Carry, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Mic;
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/247,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7167
LENGTH: 1299
TYPE: DNA
ORGANISM: Escherichia coli
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Best Local Similarity 99.5%;
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OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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Carr, Grant
Carr, Robert
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Sequence 5, Application US/09866379
Patent NO. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
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ORGANISM: Bscherichia co
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1901)
OTHER INFORMATION: n is
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               CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                  CGGCAJACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCJAACTTGTGC
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; Sequence 9, Application US/09866379

; Sequence 9, Application US/09866379

; Patent No. US20020136754A1

; GENERAL INFORMATION:

; APPLICANT: DIVERSA CORPORATION

; APPLICANT: SHORT, Jay

; APPLICANT: SHORT, Jay

; APPLICANT: BARTON, Nelson

; APPLICANT: BARTON, Nelson

; APPLICANT: GARRETT, James

; APPLICANT: GARRETT, James

; APPLICANT: DIVEN1370-7

; CURRENT APPLICATION NUMBERS US/09/866,379

; CURRENT PILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: US 09/580,515

; PRIOR APPLICATION NUMBER: US 09/580,515

; PRIOR APPLICATION NUMBER: US 09/318,528

; PRIOR APPLICATION NUMBER: US 09/291,931

; PRIOR PILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: US 09/291,931

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TYPE: DNA
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NAME/KEY: misc_feature
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          CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG
                                              GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTGTTTTGCTACAA
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GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, Nelson Robert
APPLICANT: Garyett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: ARD USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/860,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOFTMARE: FastSEQ for Windows Version 4.0
SOFTMARE: FastSEQ for Windows Version 4.0
SOFTMARE: FastSEQ for Windows Version 4.0
SOFTMARE: misc feature
NUMBER: Disc feature
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                     NAME/KEY: misc_feature
LOCATION: 403
OTHER INFORMATION: n =
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Query Match Best Local Similarity

97.2%;

Score 1284.6; Pred. No. 0;

DB 8;

Length 1901;

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21 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGC	21	Ş
1148 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1207	48 TTTA	밁
61 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAA	61 TTTA	ş
88 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 11	88 TIG	뫄
01 TIGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCCACTTCAGTACTG 96	O1 TTGA	5
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CGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG	41	Ş
8 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 10	æ	밁
1 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 8	_	ક
GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGATCACC 96	8	뮻
21 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGG	21	ş
48	48	р.
61 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTC	61 AAGG	Ş
788 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 847	88	밁
01 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACT	ដ	Ś
8 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 7	28 -	맑
41 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTG	41	S
668 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 727	83	멍
81 AACGTGACTGACGCGATCCTCAGCAGGGCAGGGAGGGTCAATTGCTGACTTTAG	81	S
608 TCCAGTCCCGATCTCTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 667	80	문
21 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 4	21 T	S
548 GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG 607	ผ	망
61	61	S
B CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 54	88	문
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428 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG 487	28	닭
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68 ACCTGGCCG	68 AC	밁
81 AC	81 AC	S
	08 GT	밁
21 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGC	21 616	S
48 TTCGCTCAGAGTGAGCCGGAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 30	13	밁
CGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTG	1	ð
8 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTTTGATTCCGTTAACCCCGCAATCTGCA 2	88	밁
CGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60		δ
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
2538, Ap	2259, Ap	17402, A	16326, A	14187, A	17, Appl	17, Appl	17, Appl	116, App	15639, A	497, App	15639, A	8976, Ap	583, App	16384, A	9082, Ap	8696, Ap	3, Appli		5, Appli	٢	z, Appii

ALIGNMENTS

Sequence 1, Application US/09259214A
Patent NO. 6110719
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVER1370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4 US-09-259-214-1 SOPTWARE: PastSEQ for Windows Version SEQ ID NO 1 LENGTH: 1323 TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc_feature
LOCATION: (1)...(1323) OTHER INFORMATION: n = A,T,C ç

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			р р	Query Match 100.0%; Score 1322; Best Local Similarity 100.0%; Pred. No. 0; Matches 1323; Conservative 0; Mismatches
CTGGCCG	GCGTGCT	CGCTCAG	GAAAGCG GAAAGCG	ilarity Conser
181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	ATGAAAGCGATCTTAATCCCATTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	100.0 100.0 vative
GGTTGGC GGTTGGC	GGCCACGC GGCCACGC	GGAGCTGA GGAGCTGA	CCCATTTT CCCATTTT	%; Scor %; Pred 0; Mi
TGACACCG	AACTGATG AACTGATG	AGCTGGAA AGCTGGAA	TATCTCTT	100.0%; Score 1322; DB 3; Length 1323; 100.0%; Pred. No. 0; 1ve 0; Mismatches 0; Indels 0;
CGNGGTGC	CAGGATGI CAGGATGI	AGTGTGGT AGTGTGGT	CTGATTCO	DB 3;
TGAGCTA	CACCCCA	GATTGTC	GTTAACC	3; Length0; Indels
ATCGCCT ATCGCCT	GACGCAT	AGTCGTC AGTCGTC	CCGCAAT	1323;
ATCTC	GGCCA 	ATGGT	CTGCA	23; 0; Gaps
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Patent No. 6183740
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 09/210,798
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
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ORGANISM: Escherichia
FEATURE:
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US-09-291-931-1

(Sequence 1, Application US/09291931A

EQUENCE 10. 6190897

(PATENT NO. 6190897

(APPLICANT: KYETZ, Keith

TITLE OF INVENTION: NOVEL PHYTASE

FILE REFERENCE: 09010/029003

(CURRENT APPLICATION NUMBER: US/09/291,931A

(CURRENT FILING DATE: 1999-04-13

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER FILING DATE: 1997-08-13

EARLIER FILING DATE: 1999-03-01

(NUMBER OF SEQ ID NOS: 4
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SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or G
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Bscherichia coli CDS (1)(1320) misc_feature (1)(1323) ORMATION: n = A,T,C or G ORMATION: n = 0, T, C or G Similarity 100.0%; Score 13 Similarity 100.0%; Pred. NG Mismat	RESULT 4 US-09-580-515-1 Sequence 1, Application US/09580515 Patent No. 6720014 GENERAL INFORMATION: APPLICANT: Kretz, Keith TITLE OF INVENTION: NOVEL PHYTASE FILE REFERENCE: 09010/029003 CURRENT FILING DATE: 1999-05-25 PRIOR APPLICATION NUMBER: US/09/580,515 CURRENT FILING DATE: 1999-05-25 PRIOR APPLICATION NUMBER: 09/318,528 PRIOR FILING DATE: 1999-05-25 PRIOR APPLICATION NUMBER: 09/291,931 PRIOR FILING DATE: 1999-04-13 PRIOR FILING DATE: 1999-04-13 PRIOR APPLICATION NUMBER: 08/910,798 PRIOR APPLICATION NUMBER: 08/910,798 PRIOR FILING DATE: 1997-08-13 PRIOR FILING DATE: 1997-08-3 PRIOR FILING DATE: 1999-03-01 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FERENCE for Windows Version 4.0	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAAGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	9y 841 CGCACGCCAGAGGTTGCCCGCAGCCCGCTAATTGGATTTTGAATCATGGAGCG 900 B41 CGCACGCCAGAGGTTGCCCGCAGCCCCGTTATTGGATTTTGATCATGGAGCG 900 B41 CGCACGCCAGAGGTTGCCCGCAAAAACAGGCGCACCCCGTTATTGGATTTAATCATGGAGCG 900 Qy 901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGGTGAACATTACCCACTTCAGTACTG 960 p01 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGGAACATTACCCACTTCAGTACTG 960 p02 961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACTGG 1020 p03 961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACTGG 1020 p04 1021 ACGCTTCCCGGTCAGCCGATAACACGCCGCCAGGTGGTGGTAACTGGAGCTCAACTGG 1020 Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGGTAACTGGTGTTTGAACGCTGG 1080 p1 1081 CGTCGGCTAAGCACGATAACACGCCGCCAGGTGGTGGTAACTGGTGTTTCAACGCTTGCACTTTAAATACAGCCTGGAGAAGCTTTACAGG 1140 pb 1081 CGTCGGCTAAGCGCATAACAGCCAGTGGATTCAGGTTGTCCAGACTTTACAG 1140 pb 1081 CGTCGGCTAAGCGCATAACAGCCAGTGGATTCAGGTTTTCCAGACTTTTACAG 1140 pb 1081 CGTCGGCTAAGCAGCAATAACAGCCAGTTGGATTTCGCTGGAGAGGTGAACTTTACAG 1140 pb 1081 CGTCGGCTGAAACAGCCAGTGGAATTCAGGTTTTCGCTGGAGAGGTGAAACTGACC 1200 1141 CAGATGCGTGAAAAAACGCCAGCTGTCATTAAATACGCCGCCCGGAGAGAGGTGAAACTGACC 1200 1141 CAGATGCGTGAAAAAACGCCACTGTCATTAAATACGCCGCCCGGAGAGAGGTGAAACTGACC 1200
	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGTTTCATTACGCAGGCATTACCATCGGAACTC Qy 601 CTTAAACGTGAGAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	361 361 421 421 481	Qy 1 ATGANAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGGCAATCTGCA 60 1

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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/319,531
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
FENCTH: 1137
                                                                                                                                                                                                           LENGTH: 1323

TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n is any nu
NAME/KEY: CDS
LOCATION: (1)...(1323)
JOTHER INFORMATION:
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Patent No. 6855365
GENERAL INFORMATION:
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                               CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1901)
OTHER INFORMATION: n is any nucleotide
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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/518,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
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PRIOR APPLICATION NUMBER: US 08/910,798
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GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
                                                                                                                                                                                                                                                                                                                                                             Query Match 97.4%;
Best Local Similarity 99.5%;
Matches 1293; Conservative
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PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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KRETZ, Keith
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                                                                                                               ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
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   Application US/09866379
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APPLICANT: GARAX, ACULIN
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GYDONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR RPILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
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NAME/KEY: misc_feature

LOCATION: (1). (1901)

OTHER INFORMATION: n is any nucleotide
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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Best Local Similarity
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Sequence 9, Application US/09866379

Patent No. 685365

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
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PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR PELLING DATE: 1999-04-13
PRIOR PELLING DATE: 1999-04-13
PRIOR PELLING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: PATENTIN VERSION 3.1
SEQ ID NO 9
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Best Local Similarity 99.4%;
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NAME/KEY: misc_feature
LOCATION: (1). (1901)
OTHER INFORMATION: n is any nucleotide
-09-866-379-9
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TYPE: DNA
ORGANISM: Escherichia coli
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                                     AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                      CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
                                                                         CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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                                                                                                                                                                                                CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAGAGGTGAAACTGACC
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ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT 1487
                                                                                                CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1447
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US-09-866-379-6

J Sequence 6, Application US/09866379

PATELICANT: NO. 6853365

GENERAL INFORMATION:
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Keith
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOCHUE, Eileen
TITLE OF INVENTION: RECOMINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7

CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli

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Matches 1290; Conserv
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                                           CGCACGCCAGAGGTTGCCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCGCGCCACCCCGTTATTAGATCATGATCATGGCAGCCGCAGCCGCAGCCCGCTTATTAGATTTGATCAAGACAGCGCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCGCGCAGCCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG
                                                                                                      GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840
                                                                                                                                       GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACC
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              TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960
                                                                                          GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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LENGTH: 1489
TYPE: DNA
ORGANISM: Escherichia
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Best Local Similarity
Matches 1280; Conservat
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                                            GGACATTACCAACGCCAGCGTCTGGTGGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG
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ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
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Sequence 9, Application US/09540149A

Patent No. 6511699

GENERAL INFORMATION:

APPLICANT: Lei, Xingen

TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY

FILE REFERENCE: 19603/2791

CURRENT APPLICATION UNMER: US/09/540,149A

CURRENT FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 60/127,032

PRIOR FILING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1
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ACCTGGCCGGTAAAACTGGGGTTGGCCTGACACCACGCGGTGGTGAGCCTAATCGCCTATCTC
                                                                                              GTGCGTGCCCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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RESULT 11

US-10-266-041A-9
; Sequence 9, Application US/10266041A
; Patent No. 6974690
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; TITLE OF INVENTION: pHOSPHATASESS WITH
; FILE REFERENCE: 19603/2798
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
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ORGANISM: Escherichia
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                 GATTCACACCAGTGGAACACCCTTGCTAAGTTTTGCATAACGCGCAATTTTTATTTTGCTACAA
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  GAAATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACT
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Qy 61 TTCGCTCAGAGTGAGCCGGAGCTGAAAGTGTGGTAATTGTCAGTCA	Query Match 95.5%; Score 1263; DB 3; Length 1486; Best Local Similarity 98.4%; Pred. No. 0; Matches 1275; Conservative 0; Mismatches 21; Indels 0; Gaps 0; Qy 1 ATGAAAGCGATCTTAATCCCATTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	; PATOK FILING DATE: 199-11-18 ; NUMBER OF SEQ ID NOS: 9 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 2 ; LENGTH: 1486 ; TYPE: DNA ; ORGANISM: Escherichia coli US-09-715-477-2	; Patent No. 6841370 ; GERRAL INFORMATION: ; APPLICANT: Lei, Xingen ; APPLICANT: Lei, Xingen ; TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE ; FILE REFERENCE: 19603/4031 ; CURRENT APPLICATION NUMBER: US/09/715,477 ; CURRENT FILING DATE: 2000-11-17 ; PRIOR APPLICATION NUMBER: 60/166,179		Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCAC 1308	QY 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	QY 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200	OY 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	Qy 961 TITATIGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020	OY 901 TIGACGCCCATCCACCGCAAAAACAGGCGTAIGGTGIGACATTACCCACTTCAGTACIG 960	Qy 841 CGCACGCCAGACGTTGCCCCCCAGCCCGCCACCCCCGTTATTGGATTTGATCATGGCAGCG 900
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; TITLE OF INVENTION: SITE-DIRECTED MUTAGENES;
; FILE REFERENCE: 19603/4031
; CURRENT APPLICATION NUMBER: US/09/715,477
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,179
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 9
; NUMBER OF SEQ ID NOS: 9
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Best Local Similarity
Matches 1268; Conserv
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SEQ ID NO 4
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ORGANISM: Escherichia
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                           AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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US-08-910-798-1

Sequence 1, Application US/08910798

PATENT NO. 5876997

GENERAL INFORMATION:
APPLICANT: KRETZ

ITILE OF INVENTION: NOVEL PHYTASE

INUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/08/910,798
FILING DATE: AUGUST 13,1997
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REPERENENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-910-798-1
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Best Local Similarity 96.1%;
Matches 1272; Conservative
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LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: PHYTASE
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               GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTTGCTACAA 840
                                                                 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
                                                                                                                  AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                                                                      CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCCATCGGAACTC
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GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                                                                                    CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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Pred. No. 0;
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-341
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US-09-489-039A-341
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Matches
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SEQ ID NO 341
LENGTH: 1266
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GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                            Local Similarity
les 202; Conserv
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                                                              GCAGCGTGCTGGAACAGTCCACCGCCAAGGCCTGGCCGCAGTGGGATGTGCCGGGCGGCC
                                                                                         CGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCAACCTGGCCGGTAAAACTGGGTT
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                                                                                                                                                                                          4.8%;
ilarity 48.7%;
Conservative
                                                                                                                                                                                          Score 63.6; DB 3;
Pred. No. 1.7e-10;
0; Mismatches 210;
                                                                                                                                                                                                                          Length 1266;
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Qy 263 TGGTAGCCGACGATTGCTGGCGAAAA	263 TGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCCGGATTA 322
263 TGGTAGCCGACGATTGCTGGCGAAAA 293 TGGCGCAGCAGAAGCTGGTGACCAGCG 323 TTGCTGATGTCGACGAGCGTACCCGTA 324 TTGCTGATGTCGACGAGCGTACCCGTA 325 ACGCTAACAGCCTGCAGCGCACCGTCG 383 CTGACTGTGCAATAACCGTACCATACCC 383 CTGACTGTGCAATACCGTACCATACCC 384 CTGACTGTGCAATACCGTACCATACCC 385 CTGACTGTGCAATACCGTACCATACCC 386 CTGACTGTGCAATACCGGTTGCCAACC 1	263 TGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTA
TGGTAGCCGACGGATTGCTGGCGAAAA	TGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTA
	AGGGCTGCCGCAGTCTGGTCAGGTCGCGATTA

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Minimum DB
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                                                                                                                                                                                                                                                                                      Score
    seq length: 0
seq length: 2000000000
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1308
1 atgaaagcgatctt
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1. /EMC_Celerra_SID83/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2. /EMC_Celerra_SID83/ptodata/2/pubpna/US07_NEW_PUB.seq:*

3. /EMC_Celerra_SID83/ptodata/2/pubpna/US08_NEW_PUB.seq:*

4. /EMC_Celerra_SID83/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

5. /EMC_Celerra_SID83/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6. /EMC_Celerra_SID83/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7. /EMC_Celerra_SID83/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8. /EMC_Celerra_SID83/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                     Query
Match Length
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7741.348 Million cell updates/sec
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   atgaaagcgatcttaatccc.....gcagtttgagatctcatcta 1308
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   GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration
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 US-10-449-902-6979
US-11-237-529-79920
US-11-293-697-2180
US-10-953-349-11004
US-10-953-349-27515
US-10-449-902-13863
US-10-449-902-15013
US-10-449-902-15013
US-10-449-902-15013
US-10-449-902-965
US-10-449-902-12803
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US-10-449-902-12803
US-10-449-902-25657
US-10-449-902-25657
US-10-449-902-25657
US-11-217-529-80383
US-10-449-902-2911
US-10-449-902-2911
US-10-449-902-2911
US-10-449-902-21266
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8987, Ap
13868, A
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1501, App
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1502, App
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atc cal 11 17 64 17 58 52 3	SULT 1 10-449-902-697 Sequence 6979, Publication No. GERMERAL INFORMA APPLICANT: BA APPLICANT: BA APPLICANT: BI APPLICANT: FO TITLE OF INVEN TILE REFERENCE CURRENT FILING PRIOR APPLICAT PRIOR APPLICAT PRIOR FILING D	888 NN
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	SULT 1 10-449-902-6979/c 10-449-902-6979/c 10-449-902-6979/c Sequence 6979, Appli Publication No. US20 GENERAL INFORMATION: APPLICANT: Bio-ori APPLICANT: Bio-ori APPLICANT: Foundat APPLICANT: FOUNDAT APPLICANT: FOUNDAT PILE OF INVENTION: FILE REFERENCE: MOA CURRENT FILING DATE: FRIOR APPLICATION N PRIOR APPLICATION N PRIOR FILING DATE: PRIOR APPLICATION DATE: PRIOR FILING DATE: PRIOR APPLICATION IN PRIOR DATE: PRIOR FILING DATE	000000000000000000000000000000000000000
larity Conserva GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	02-6979/c 02-6979/c 02-6979, Applicat on No. US20060 NFORMATION: T: National IT T: Bio-orient T: Bio-orient T: Foundatior T: Foundatior INVENTION: FR RENCE: MOA - AA PELICATION NUME FILING DATE: 200 FILING DATE	******************
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core red. Mis AAGGC AACGA CTGGG TTTCCT CAGCGC CAGCGC	9902 Agrobiological gy Research Ad ical and Chemi ement of Inter LANT CDNA AND /449,902 -203269 -383870	US-11-154-977 US-11-154-977 US-11-154-977 US-11-154-977 US-11-154-977 US-11-154-977 US-10-449-902 US-10-449-902 US-10-449-902 US-10-449-902 US-11-121-154 US-11-217-529 US-11-217-529 US-11-23-697 US-10-449-902 US-11-249-902 US-11-293-697 US-10-449-902
dre 37.6; d. No. 0.0 Mismatches GGCCACGCAC GGGTGAGCTG CCTGGAGATG CCTGGAGATG GGGTCTGGTA GGGTCTGGTA ACCTCTGCAC	02 robiolo Resear ent of ent of A9,902 03269 83870	GNN 4449317119494
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2.9%; Score 37.6; DB 6; Length 1627; imilarity 50.6%; Pred. No. 0.0073; ; Conservative 0; Mismatches 89; Indels 0; Gaps carggrangergerceaaccaagecaaccaagecaageargerceaaccaagea [Institution ch. cience. OF	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
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0 174 586 234 234 294		Appl Appl Appl Appl Appl Appl Appl Appl
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RESULT 2 US-11-217-529-79920/c ; Sequence 79920, Application US/11217529

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PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2180
LENGTH: 2879
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-2180
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APPLICANT: NAKANORA, YOSHIHIRO
APPLICANT: NAKANORA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GEI
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
INUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79920
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
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Best Local Similarity
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CURRENT FILING DATE: 2005-12-05
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268
                                                                                                                     194 AACTGGGTGAGCTGACACCGCGCGGGGGGGGGAGATCGCCTATCTCGGACATTACTGGC
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                                                                                GCATGGTGTGGCGGAAGTCGCCCAGCGGGGCGCTGATCATCTCGGCCGTGAGGTCCGCTC
GGGAACGGCGCTTGGAGTGCACCGAGCTGGACACCAGTTGCT 227
                                       GTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCT 295
                                                                                                                                                                CCGCGGCCTTGCTATTGAGGAAGGAGGTGTCCCCAAAGGCGTCTCCGGCCCGGCCAACGT
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Pred. No. 0.061;
0; Mismatches
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Pred. No. 0.19;
0; Mismatches
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RESULT 4

RESULT 6 US-10-449-902-8987

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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 11004
LENGTH: 2271
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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; ORGANISM: Triticum aestivum
US-10-953-349-27515
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US-10-953-349-27515/c
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Publication No. US20060107345A1
GENERAL INFORMATION:
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27515
                                                                                                                                                                                                                                                                                                                        Query Match 2.5%;
Best Local Similarity 48.4%;
Matches 90; Conservative
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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987
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                                                                                                                                                                                                     GGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGA 722
                                        TTCACA 788
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                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13868
LENGTH: 2634
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                                                                                                   Query Match
Best Local
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LENGTH: 1396
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                                                                                                                                                                                                TYPE: DNA
ORGANISM: OTYZA BALIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK111216
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
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ORGANISM: OTYZA BATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK106335
DATABASE ENTRY DATE: 2002-08-28
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APPLICANT: Bio-oriented Technology Research Advancement Institute APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-USE
FILE REFERENCE: MOA-A0205Y1-USE
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
COETUNES: 56791
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199 GGTGAGCTGACACCGCGCGGTGGTGAGCTAATCGCCTATCTCGGACATTACTGGCGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456
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                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTCGTTCTCGGTCGCCGTCGCCTTCTCGCCGAAGCGGAGGAGCTCGTACTCCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTCTCCTGCAA
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                                                                                                   2.4%;
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                                                                          Score 31.8; DB 6;
Pred. No. 1.1;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 6
Pred. No. 0.63;
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                                                                                                                        Length 2634;
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                                                                   RESULT 9
US-10-449-902-10760/c
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US-10-449-902-13863/c
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
CURRENT FILING DATE: 2003-05-29
GENERAL INFORMATION:
                       Sequence 10760, Application US/10449902
Publication No. US20060123505A1
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SEQ ID NO 13863
LENGTH: 3129
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Best Local :
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK111211
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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Local Similarity 47.7%;
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                                                                                                                                                                                                                           GCCCGGAGAGGTG 1191
                                                                                                                                                                            ACCAGGAGTGCTG 2750
                                                                                                                                                                                                                                                                            GGTGAACCCGGAGATGTTGGAGAGCÁTGGAGGAGGAACGGCCGCGGCCATTGCGGAGGGA
                                                                                                                                                                                                                                                                                                                      GCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCC 1178
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Pred. No. 1.7;
0; Mismatches 101;
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.

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US-10-449-902-15013
; Sequence 15013, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-293-697-707
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SEQ ID NO 707
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.
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TYPE: DNA
ORGANISM: Oryza sativa
ORGATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108108
DATABASE ENTRY DATE: 2002-08-28
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                                                                                                                                                                                                                                            1359
                                                                                                                                                                                                                                                                                                                                           1419 CCTTCGCAGTGAGTGTTACAGCTCTTAAGGCGGTGTGTCTGGAGTTGTTCATTCCTCCTG
                                                                                                                                                                                                                                                                                           119 GTGTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 GCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCGCAGTCTGGTCAGGTCGC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 TGŤTGŤTĠĊCĠTTĠŤĊĠĀĊĠĀĠĠĠĀGTĊGCCGĀĀCĀCĠĀĀĠĀĀĠĠĊCCGCTČCGĊĠĠĀĊ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 GATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAAGCCTTCGCCGGCGGGC 376
                                                                                                                                                                                                                                                                                                                                                                                     59 CATTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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llarity 55.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 2791;
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; TYPE: DNA
; ORGANISM: OTYZA SATÍVA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK065548
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-15013
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US-10-517-441-65/c
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SEQ ID NO 15013
LENGTH: 3553
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Best Local Similarity
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APPLICANT:
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TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
                         APPLICATE: HORFIER, Heiler
APPLICANT: HORFIER, Heiler
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast of title OF INVENTION: Method and nucleic acids for the improved treatment of breast of title OF INVENTION: Method and nucleic acids for the improved treatment of breast of title OF INVENTION INVEST: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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OF SEQ ID NOS: 2147
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SCHMITT, Manfred
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Pred. No. 3;
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RESULT 14
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US-10-449-902-965/c
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Sequence 18030, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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Best Local S
Matches 60
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LENGTH: 3050
TYPE: DNA
ORGANISM: Homo Sapiens
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Publication No. US20060123505A1
GENERAL INFORMATION:
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK059042
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: Patentin Ver. 2.1
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Pred. No. 1.3;
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US-11-289-102-50/c
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TYPE: DNA
ORGANISM: OTYZB SBITYB
ORGANISM: OTYZB SBITYB
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK068443
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18030
                                                                                                                                                                                     TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS FILE REFERENCE: 10338 NP CURRENT APPLICATION NUMBER: US/11/289,102 CURRENT FILING DATE: 2005-11-29 PRIOR APPLICATION NUMBER: US 60/631,993 PRIOR FILING DATE: 2004-11-30 PRIOR FILING DATE: 2004-11-30 PRIOR PRIOR DATE: 2004-13-30 SEQ ID NOS: 395 SOFTWARE: Patentin version 3.3 SEQ ID NO 50 LENGTH: 3452
                                                               Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50, Application US/11289102
Publication No. US20060121511A1
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SEQ ID NO 18030
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APPLICANT: Shaw, Peter M.
APPLICANT: Clark, Edwin
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR TILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION STATE OF SEQ ID NOS: 56791
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                               Local
997 GGCGGCGCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCCAGGT 1056
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ilarity 45.3%;
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Pred. No. 1.9;
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Qy 1057 GGTGAACTGG 1066 	1057
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Thu Jun 15 11:39:03 2006

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match Best Local Similarity

45.3%; 97.6%;

Score 592; DB 2; Length 616; Pred. No. 4.9e-175;

ALIGNMENTS

/mol_type="marky" /mol_type="marky" /db xref="taxon:8355" /clone="XL090]06" /tissue_type="whole embryo" /tissue_type="whole embryo" /dev_srage="stage 25" /clone_lib="NIBB Mochii normalized Xenopus tailbud library"	ORIGIN
http://xer I 1	FEATURES source
National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp The information of this clone is available through the following URL.	
K.L. Ayama, A., Terabaka, C., MOCDII, M., Ueno, N., Shin-1, T. and Kohara, Y. Kohara, Y. Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i Contact: Tadasu Shin-i	TITLE JOURNAL COMMENT
	REFERENCE
B0074127.1 GI:17504316 BST. Kenopus laevis (African clawed frog)	VERSION VERSION KEYWORDS SOURCE ORGANISM
	RESULT 1 BJ074127/c LOCUS DEFINITION

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REFERENCE
AUTHORS
TITLE
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                    Fax: 0
Email:
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AppaDB: an AcedB database
Pristionchus pacificus
                                            Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                 Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                      Contact: Sommer RJ
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1: ralf.sommer@tuebingen.mpg
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                                                                                                  CA093060
SCCCCL2001D10.b CL2
3', mRNA sequence.
CA093060
CA093060.1 GI:3494
EST.

Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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Class: fosmid ends.
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                             AGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT
                                                                                                                                   CCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGA
                                                                                                                                                                 CCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAGA
AGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
                                                                  GGTGAAACTGA
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/mol_type="genomic_DNA"
/strain="California"
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var. California"
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GI:34946367

CL2

Saccharum

746 bp mRNA marum officinarum

CDNA

clone SCCCCL2001D10

EST 23-SEP-2003

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Best Local Similarity
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Fax: 55 19 3788 1139
Fax: 55 19 3788 1089
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Plate: 001 row: D column: 10
Seq primer: M13/Forward primer.
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Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vettore,A.L., da Silva,F.R., Kemper,E.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                       CTACAACGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAG
AACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAA
                                                                                               GTGCTGTTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTC 1014
                                                                                                                                                                                     ACAGCGTTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGACATTACCCACTTCA 954
                                                                                                                                                                                                                              CTACAACGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="CL2"
/clone lib="CL2"
/note="Organ: Pool of sugarcane calli submitted to low
(4oC) and high (37 C) temperature stress; Vector:
pslurScript; Site 1: EcoRI; Site 2: XhoI; An
unidirectional cDNA library generated from [Pool of
sugarcane calli submitted to low (4oC) and high (37 C)
temperature stress]. CDNA was prepared from polyA+ mRNA
using ZAP - cDNA Synthesis Kit (Stratagene). The
double-strand cDNAs were fractionated in a sepharose CL-2B
40cm-columns and fragments sizing between 0.8 and 1.5 Kb
were directionally cloned into the vector. Details of
each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Saccharum officinarum"
/mol type="mRNA"
/db_xref="taxon:4547"
/clone="SCCCCL2001D10"
/lab_host="XL1Blue MRF/"
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Pred. No. 7.3e-156;
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BU713770
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Schistosoma japonicum
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 529)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Wang,S.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
Evolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 86-21-50801919(ex.45)
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/note=Tvector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2: //note=Tvector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2: //note=Tvector: Lambda ZAP-II XR.; Schietosoma japonicum (Anhui, P.R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRNA was isolated at the QIMR from lysates of these worms by oligo dT chromatography, using a kit from pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dT-XhoI-primer and synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to EcoRI linkers, digested with EcoRI and XhoI, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QAMR. During analysis of the library at the QIMR, we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Schistosoma japonicum"
/mol type="mRNA"
/strain="Chinese (Anhui) strain"
/db xref="taxon:6182"
/sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
/clone_lib="Adult SjC 7/94"
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Road, Zhangjiang Hi-Tech Park, Pudong,
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                                                                                    1 (bases 1 to 595)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnollophyta; Liliopsida;
Clade; Ehrharroideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                  CF326092 595 bp mRNA linear EST 18-
JWT1--05-B09.g1 AtJWT-overexpressing transgenic rice lambdd
cDNA library (JWT1) Oryza sativa (japonica cultivar-group)
clone JWT1--05-B09, mRNA sequence.
Genomics and Genetics Institute, GreenGene Biotech I of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                    Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                            CF326092.1 GI:33800445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGA 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."
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Pred. No. 1.3e-153;
0; Mismatches 3;
                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
a; Poales; Poaceae; BEP
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                                          Biotech Inc.; Division
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POCUS

COMMENT

TITLE AUTHORS

REFERENCE

KEYWORDS

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KEYWORDS
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                                               VERSION
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    ORGANISM
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Best Local
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IDOAAASDCO9RMI F

MRNA sequence.

CN762997.1 GI:4

EST.

Acyrthosiphon pi

Acyrthosiphon pi
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                                                                                                                                                                                                                                                                                                                  TTAAATACGCCGCCCGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 31 330 6193
82 31 321 6355
l: bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone_lib="B.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JWT1--05-B09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa
                                               GI:47536920
   pisum
pisum
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                                                                                          ApMS
                                                                                          Acyrthosiphon
                  (pea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 488.2; DB 5;
Pred. No. 3.1e-142;
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                                                                                                        895
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                                                                                         mRNA linear
pisum cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 485;
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UMR B103P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope

PCR PRImers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Parameoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (Dases 1 to 895)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 5 row: C column: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An expressed sequence tags database for the pea aphid Acyrthosiphon
TACGCCGCCCGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGG 1232
                                                                                     GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCATCCACCGCAAAAACAGGCGTA
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                                                     GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA
                                                                                                                                                            AGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA
                                                                                                                                                                                                 AGGTGGTGAACTGGTGTTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA 1112
                                                                                                                                                                                                                                                                                                                           TCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCCCCGGTCAGCCGGGATAACACGCCGCC 1052
                                                                                                                                                                                                                                                                                                                                                                                 TGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
/note="Vector: pBS-SK minus; Site 1: EcoRI; Simple name: IDDARA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: (0)(6/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XI1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Acyrthosiphon pisum"
/mol type="mRNA"
/cultivar="developmentstage"
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/clone="IDOAAA5DC09"
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99.4%;
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Matches 459;

Similarity

Conservative

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Gaps

898 810

839 AACGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAG

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VERSION
KEYWORDS
SOURCE
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CN754382/c
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                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 868)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon
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CN754382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aph. Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMR BiO3P, BP 35327, F
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
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FORWARD: CAGGAMACAGCTATGACC
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                                                                                                       /clone_lib="ApMS"-
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
Sample name: IDOAPA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 00/6/1999;
Soil conditions: Soil; Sowing date: 00/6/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction: ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
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/cultivar="developmentstage"
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                        34.2%;
99.4%;
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Score 446.8; DB 8;
Pred. No. 4.2e-129;
D; Mismatches 2;
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JOURNAL COMMENT
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
                                                                                                                                                                                                                                 (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                    Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyr
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CN757565
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                                                                                                                                                                                      FORWARD: CAGGAAACAGCTATGACC Plate: 1 row: F column: 9.
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               /clone="IDOAAA1DF09"
/tlssue type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic
/lab host="XI1-Blue"
/clone_lib="ApMS"
                                                                                                                                                                      Location/Qualifiers
/clone_lib="ApMs"
/note="Vector: pBS-SK minus; Site_1:
                                                                                            cultivar="developmentstage"
db_xref="taxon:7029"
                                                                                                                          organism="Acyrthosiphon pisum"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                    pea aphid Acyrthosiphon
    EcoRI; Site_2: XhoI
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Matches 455;
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CGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
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                                                                                                GGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTTACGCAAAT 1262
                                                                                                                                                                                                        GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACCCT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                            GCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCTGGCG 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGCCCATCCACCGCAAAAACAGGCGTATGGTGACATTACCCCACTTCAGTGCTGTT
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                                                                                                                                                                      GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACCCT
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                                                              GGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ecology & Evolutionary Biology, Princeton University; soil conditions: Soil; Sowing date: 01/66/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
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Pred. No. 7.7e-128;
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PUBMED COMMENT
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ORGANISM
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                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                           AUTHORS
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicotyledons, Spermatophyta, Magnollophyta, eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                        Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
                                                                                                                                     1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone M11B12 5', mRNA sequence BE520240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE520240 393 bp mRNA linear EST 19-MAR-2001 M11B12STM Arabidopsis developing seed Arabidopsis thaliana cDNA
Michigan State University
224 Biochemistry, Michiga
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  Michigan
  State University,
     East
  Lansing,
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RESULT 10
AW036132
LOCUS
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ORGANISM
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Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta, Magnoliophyta; eudicotyledons; Core eudicotyledons;
Lycopersicon.

1 (bases) lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases) 1 to 383)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,P., Upton,J., Ronning,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C.,
                                                                                                                                                                                                                                              AW036132

383 bp mRNA linear EST 18-MAY-200 EST274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEE1823 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036132
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Fax: 517 353 9334

Email: benning@meu.edu

Michigan State University DNA Sequencing Facility Arabidopsis

Biological Resource Center, The Ohio State University, 309 Botany

Zoology Eddg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
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/mol type="mRNA"
/ecoType="Columbia"
/db_xref="taxon:3702"
/clone="M11812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: p
Site_1: EcoRI; Site_2: XhoII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
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Pred. No. 5.4e-106;
O; Mismatches 13;
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ACCESSION VERSION KEYWORDS

EST AW036134.1

GI:5894813

SOURCE ORGANISM

Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

LOCUS DEFINITION RESULT 11 AW036134/c

AW036134
383 bp mRNA linear EST 18-MAY-2001
EST274510 tomato seed, TAMU Lycopersicon esculentum cDNA clone
cLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase
precursor, putative, mRNA sequence.
AW036134

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Best Local Similarity
Matches 375; Conserv
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JOURNAL
361
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ATCAATGCTGACGGAGATATTTC
                   ATCAATGCTGACGGAGATATTTC
                                                          ACCATCGGAACTCAAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGC
                                                                                                                        ATCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="quiescent seed"
/lab_host="XL1-Blue MRF'"
/clone_lib="tcomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Sit
Xho1; cLEE - Tomato Seed EST Library. Directionally
cDNAs inserted into pBlueScript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
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/tissue_type="seeds"
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                                                                         BU713769 Adult SjC 7/94 Schistosoma japonicum cDNA similar to spipo71.02|ppA BCOLI PERLPLASMIC APPA PROTEIN PRECURSOR [INCLUDES: PHOSPHOANHYDRIDE PHOSPHOHYDROLASE (PH 2.5 ACID PHOSPHATASE) (AP);
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                                                         6-PHYTASE ], mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xhol; cLEB - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBlueScript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="seeds"
/dev_stage="quiescent_seed"
/lab_host="XL1-Blue_MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4081"
/clone="cLEB1E23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
cultivar="TA496"
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                    GI:28321125
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97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 370.2; DB 7;
Pred. No. 5.5e-105;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
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                                                                                                                                      EST 23-OCT-2003
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δ 문 ફ 밁 S

CTCCTGCAACAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGGATCACCGATTCACAC 789 CTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACAC 120

61

Matches

Local Similarity 425;

Conservative

ç

Mismatches

Indels

4.

Gaps

4

GCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT

GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG 60

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                                                                                                                           Query Match
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1 (bases 1 to 531)

Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., Xu,X.N., Wang,Z.Q., Wang,Z.Q., Shang,X.L., Wang,Z.Q., Brindley,P.J., Xu,X.N., Wang,Z.Q., Wang,Z.Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schistosoma japonicum
Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementary DNA resource
                                                                                                                                                                                                                                                                                                                                                                                        /db xxef="taxing (minut) strain (db xxef="taxing (minut) strain (db xxef="taxing (minut) strain (db xxef="taxing (minut) strain (minut) strai
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                                                                                                                                                                                                                                                                                                                                                         Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Schistosoma japonicum"
/mol_type="mRNA"
/strain="Chinese (Anhui) strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                        Japonicum
                                                             26.7%;
                                                                   Score 348.6;
Pred. No. 4.1
                                                                                                                                                                                                                                                                                                        sequences
4.1e-98;
ches 54;
                                                                                                                           DB 3;
                                                                                                                     Length
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CN759004/c
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KEYWORDS
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5', mRNA sequence.
CN759004
CN759004.1 GI:47532927
                                                                                                                                                                                                                                                                                                                                                                                              PCR PRIMETS
FORWARD: CAGGAAACAGCTATGACC
Plate: 24 row: C column: 4.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Acyrthosiphon pisum
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Paraneoptera, Hemiptera, Sternorrhyncha, Aphidiformes,
Aphidoidea, Aphididae, Macrosiphini, Acyrthosiphon.
1 (bases 1 to 706)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMR BiO3P, BP 35327, FTel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2004)
Contact: D. Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC
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/mote="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
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| clone="IDAAA24BC04"
| /tissue_type="whole insect"
| /dev stage="nymphs and adults (parthenogenetic females)"
| lab_host="XXI-Blue"
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Local Similarity
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                                          GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                                                                                                                                                                                                                                                                                                                                                               ACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCT
GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
                                                                                                                                                                               CGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTC 1241
                                                                                                                                                                                                                                                GGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCC
                                                                                                                                                                                                                                                                                                          GGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCC 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCACTGGAGCTCAACTGGACGCTTCCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGA
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99.3%;
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Pred. No. 2.1e-81;
0; Mismatches 2;
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Email: libin@helix.nih.gov Seq primer: M13 Reverse. Location/Qualifiers Hominidae; Homo.

1 (bases 1 to 354)

1 (bases 1 to 354)

1 (bases) F., Young, M., Schuler, G., Powell, J., Yang, L., Jia, L., Robey, P., Young, M., Bowles, L., Geisel, S., Kucaba, T., Lennon, G., Hiller, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Marra, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., Wylie, T., Waterston, R., Wilson, R. and Francomano, C. WashU-MGB/NHGMI EST Project

WashU-MGB/NHGMI EST Project

Unpublished (1997) AA545747

ABS457184-REV Human Bone Marrow Stromal Fibroblast Homo sapiens clone HBMSF1B4 5', mRNA sequence. AA545747 AA545747.1 GI:2307026 Tel: 301-402-4877 Fax: 301-496-7157 National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda, Contact: Libin Jia Medical Genetics Branch Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human) /tissue_type="bone marrow" /cell_type="stromal fibroblast" /dev_stage="mixed" /lab_host="XL1-Blue" organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" clone="HBMSF1B4" sex="Male and Female" . 354 ₹ 20892-1267, EST 12-MAY-1999 omo sapiens cDNA

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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              707 bp mRNA linear EST 01-OCT BJ619443 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL189d24 5', mRNA sequence. BJ619443
                                                                                                                                                                                                                                                                    Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 707)

1 (bases 1 to 707)

1 (kases 1 to 707)
                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                           Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                              http://xenopus.nibb.ac.jp.
                                                                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                Kohara,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
Xenopus laevis
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/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI"
                             /organism="Xenopus laevis"
/mol_type="mRNA"
/db xref="taxon:8355"
/clone="XL189d24"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early
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 AAATCTCGGCGGCGCA
                    AAATCTCGGCGGCGCA 1005
                                                 GTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGC
                                                                                                    CACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAGGC
                                                                                                                            CACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAACAGGC 929
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Pred. No. 2.6e-68;
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Search completed: June 14, 2006, 14:21:52 Job time: 6872.62 secs

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Minimum DB n
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Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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10064.996 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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         3 10 US-10-933-115-9
3 14 US-11-56-354-1
5 US-10-601-319-6
8 US-10-601-319-5
10 US-10-601-319-5
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3 US-09-866-379-1
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US-10-601-319-9
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Sequence 1, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 3, Appli
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12.6	12.6	12.6	12.6	14.6	16.2	17.0	17.3	17.6	28.8	28.8	28.8	30.9	52.8	52.9	52.9	58.0	93.5	93.5	93.9	93.9	94.3	96.5	96.5	96.6	96.6	96.6	96.6
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304,		302,	Sequence 301, App	e 25	μ.		Sequence 3, Appli	1608,				Sequence 3181, Ap	e N	4.		ŗ	e 4	4	Sequence 1, Appli	•	(D (2)	Sequence 9, Appli	5	Ψ	Sequence 7, Appli	Sequence 6, Appli	Sequence 7, Appli

ALIGNMENTS

RESULT 1 US-10-156-660-1

Sequence 1, Application US/10156660 Publication No. US20030103958A1

GENERAL INFORMATION:

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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
PILE REFERENCE: 09010-029007
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER
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Best Local Similarity
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                                                                                                                                    GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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             TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
                                             TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
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                                                                                         CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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  TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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                                                                              Local Similarity
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APPLICANT: Kretz, Keith A.

APPLICANT: Kretz, Keith A.

APPLICANT: Gray, Kevin A.

APPLICANT: Gray, Kevin A.

APPLICANT: Gray, Kevin A.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Gorrett, James B.

APPLICANT: O' Donoghue, Eileen

APPLICANT: O' Donoghue, Eileen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: RECOMBINANT PHYTASES AND MET

TITLE OF INVENTION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/292,214

PRIOR APPLICATION NUMBER: US 08/910,798

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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified phytase er
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1296)
                                                                                                                      ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCCGCAATCTGCA
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FILE REFERENCE: 564462001822

CURRENT EJLING DATE: 2004-09-01

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR PILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR PILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR PILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOPTWARR: FRASTSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1308
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Publication No. US20050281792A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
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US-10-933-115-9
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 1308
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APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
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ORGANISM: Artificial Sequence
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCTA 1308
                                                                                                                                                    CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200
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                                                                                  CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260
                                                                                                                                   CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC
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WESULT 4
US-11-056-354-1
Sequence 1, Application US/11056354
Publication No. US20050246780A1
Publication No. US20050246780A1
GENERAL INFORMATION:
APPLICANT: SHORT, Jay M.
APPLICANT: SHORT, Veith
APPLICANT: GRAY, Kevin A.
APPLICANT: GARRETT, Keith
APPLICANT: GARRETT, James B.
APPLICANT: GARRETT, James B.
APPLICANT: O'DONOGHUE, Bileen
APPLICANT: O'DONOGHUE, Bileen
APPLICANT: O'DONOGHUE, BILEEN
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 564462001803/D1370-9C1
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/880,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1296
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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Best Local Similarity
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  GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                               GCCTTCGCCGCCGGGCTGGCACCTGTGCAATAACCGTACATACCCAGGCAGATACG
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RESULT 5
US-10-601-319-6
; Sequence 6, Ap
Sequence 6, Application US/10601319
Publication No. US20040091968A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
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SENGTH: 1901
LENGTH: 1901
TYPE: DNA
CORGANISM: Escherichia coli
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 403
OTHER INFORMATION: n = A,T,C or
US-10-601-319-6
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CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT FILING DATE: 2003-06-20

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 2001-05-24

PRIOR PRICING TO AUTHORISE: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR PRICING DATE: 2000-05-25

PRIOR FILING DATE: 1990-05-25

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR PRILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10
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                  CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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Sequence 5. Application US/10601319

Publication No. US20040091968A1

GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Welson Robert
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
FILTE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
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PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
INUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1901
TYPE: DNA
ORGANISM: Bscherichia coli
PEATURE:
NAME/KEY: misc_feature
LOCATION: 403
COTHER INFORMATION: n = A T C or G
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                                                                                                                                                                                                                       CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT PILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
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US-10-933-115-5
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564422001822
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; LOCATION: 403
; OTHER INFORMATION: n =
US-10-933-115-5
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Qy 121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	Qy 61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	QY 1 ATGAAAGCGATCTTAATCCCATTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	Query Match 96.7%; Score 1265; DB 3; Length 1323; Best Local Similarity 98.0%; Pred. No. 0; Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	; NAME/KEY: misc_feature ; LOCATION: (1):-(1323) ; OTHER INFORMATION: n is any nucleotide US-09-777-566A-1		39 PP	PRIOR FILING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: US 08/910, PRIOR FILING DATE: 1997-08-13 NIMBER OF SEO ID NOS.	- ω	,566A 28	APPLICANT: DIVERSA CORPORATION APPLICANT: SHORT, Jay APPLICANT: KRETZ, Keith TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THERROF	US-09-777-566A-1 ; Sequence 1, Application US/09777566A ; Patent No. US2001005578BA1 . GENERAL TURPOMATION.	8	Db 1388 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1447 Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300	1201 CTGGCAGGATGTGAAGAGGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA	QY 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200	1268 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG	1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG	QY 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	QY 961 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020
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Sequence 1, Application US/09866379
Patent No. US20020136754A1

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: O'DONOGHUB, Elleen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PH)
FILE REFERENCE: DIVER1370- US/09/866,379
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN PATENTIN SEQ ID NOS: 10
SOFTWARE: PATENTIN SEQ ID NOS: 10
SOFTWARE: PATENTIN SEQ ID NOS: 10
SUBJECT OF SECURITY OF SE
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US-09-866-379-1
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LOCATION: (1)...(1323)
OTHER INFORWATION: n is any ni
NAME/KEY: CDS
LOCATION: (1)...(1323)
OTHER INFORWATION:
US-09-866-379-1
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Best Local Similarity 98.0%;
Matches 1280; Conservative
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ORGANISM: Escherichia coli
FEATURE:
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j Sequence 1, Application US/10034985
j Publication No. US20030049815A1
j GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/034,985

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: US/09/580,515

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: 09/259,214

PRIOR APPLICATION NUMBER: 09/259,214

PRIOR APPLICATION NUMBER: 09/259,214

PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1323

TYPE: DNA

ORGANISM: Escherichia coli
FEATURE:
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc_feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or
JS-10-034-985-1
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SEQ ID NO 1
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Best Local :
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                                                        CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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                    CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                           TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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98.0%;
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US-10-430-36-1
US-10-430-356-1
US-10-430-356-1
; Sequence 1, Application US/10430356
publication No. US20030232041A1
; GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/02903
; CURRENT APPLICATION NUMBER: US/10/430,356
; CURRENT FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 09/299,214
PRIOR PILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; ORGANISM: Escherichia coli

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Best Local Similarity
Matches 1280; Conserv
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NAME/KEY: misc_feature

LOCATION: (1)...(1323)

OTHER INFORMATION: n = A,T,C

-10-430-356-1
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                                        CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG
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RESULT 12
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TITLE OF INVENTION: RECOMBINANT PHYTASES AND
TITLE OF INVENTION: RECOMBINANT PHYTASES AND
TITLE OF INVENTION: RAD USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/880,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SECTION NOS.
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Publication No. US20040091968A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows
SEQ ID NO 1
 Query Match
                                                                                                                                                                     LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia c
FEATURE:
                                                 PEATURE:
NAME/KEY: misc_feature
LOCATION: 216
OTHER INFORMATION: n = 1
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APPLICANT:
APPLICANT:
                                                                                                                                 NAME/KEY: CDS
LOCATION: (1)...(1320)
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Garrett, James B.
O' Donoghue, Eileen
Mathur, Eric J.
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ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
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FILER REFERENCE: 56446201822
CURRENT FILING DATE: 2004-09-01
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/09/886,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
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PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/295,214
PRIOR APPLICATION NUMBER: US 09/295,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR PRIOR DATE: 1997-08-13
PRIOR PRIOR DATE: 1997-08-13
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson I.
APPLICANT: Barrett, James I.
APPLICANT: O' Donoghue, Eil
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US-10-933-115-1
; Sequence 1, Application US/10933115
; Publication No. US20050281792A1
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Best Local Similarity
Matches 1280; Conserv
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LENGTH: 1323
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Escherichia c
FEATURE:
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LOCATION: (1)...(1320)
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APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 216
OTHER INFORMATION: n =
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                                                                 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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Sequence 7167, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
APPLICATION: Identification of Essential Gen
FITLE OF INVENTION: Identification of Essential Gen
FITLE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7167
LENGTH: 1299
TYPE: DNA
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Best Local Similarity
Matches 1276; Conserva
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Escherichia
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Zyskind, Judith
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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
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OTHER INFORMATION: n is any nucleotide
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US-09-866-379-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09866379 Patent No. US20020136754A1 GENERAL INFORMATION:
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Best Local S
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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TYPE: DNA
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                            CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA 360
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421 TCCAGITCCCGATTCCGTTATTTAATCCTCTAAAAACTGGGGTTTGCCAACTTGGCAATTGGCAACTTGGCATATAAACTGGGGTTTGCCGAACTTGGCAACTTGGCATATAAACTGGGGTTTGCCGAACTTGGATATAACTGGGGTTGACTTTACCGGATTGGTAACTTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTTTACCGGATTGACTATACCGAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTTACCAATTACCAATTACCAACTAAACTTTACCAACTAAACTACAACTAAACAAC
421 TCCAGGTCCGANTCGGTHATTHANTCCTCTHANNACTGGGGTTTGCCAACTGGATHA 608 TCCAGGTCCCAACTGGTHATTHANTCCTCTHANNACTGGGGTTTGCCAACTGGATHA 608 TCCAGGTCCCAACTGGTHATTHANTCCTCTHANNACTGGGGTTCATTTGCTGACTTTACCGA 608 TCCAGGTCCTGACGGATTCCTCAGAGAGGGGGGGAGAGAGGGGTCAATTGCGGATTTACCGG 608 AACGTGACTGACGGGATTCCTCAGAACTGGAACGGGTGCTTAATTTTCCGCAATTACCAACTT 728 CGGCAAACGGGGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATTACCATCGAT 601 TATCAAACGGCGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATTACCATCGAT 728 CGGCAAACGGCGACTGTTCCTCCATTAACCGGTGCGTTAACCTTCCATCAACCT 601 AACGTGAACCGCGACTGTTCCTCCATTAACCGGTGCGTTAACCTTCCATCAACCT 721 GAGATATTTCTCCTGCAACAAGCACAAGCACAGGAATTGCATTACCATCAAGCA 722 GAGATATTTCTCCTGCAACAAGCACAGGAATTGCATTACCGAGGAATTTTATTTTCCT 723 GAGATATTTCTCCTGCAACAAGCACAGGAATTTGCATTAAGGTTTGCATTAAGGTTTGCAATTTTCAATTTTCCTCTGCAACAACAAGCACTTTGCATTAAGGTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT
421 TCCAGTCCCGATTCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAAAACTGGATTACCCAACTGGATAAAACTGGATTACCCAACTGGATAAAAACTGGATTACCCAACTGGATAAAAACTGGATTACCCCAACTGGATAAAAACTGGATTACCCCAACTGGATAAAAACTGGATTACCCCAACTGGATACTGAAAAACTGGAACTGAAAACTGGAACTGAAAACTGGAACTGAAACTGGAACTGGAACTGAAACTGGAACTGAAACTTAACCATCAACTTACCAACTTACCAACTTACCATCAACTTACCAACTTAAACGTGAAAACAAGACAACAACAACAACAACAACAACAACAACAA
421 TCCAGTCCCGATCCGTTAATTAATCCTCTAAAAACTGGGGTTTGCCAACTGGATAAACTGGGGTTTGCCAACTGGATAAACTGGGGTTTGCCAACTGGATAAACTGGGGTTTGCCGAACTGGATAAACTGGATAACTGGGATAACTGGATAACTGGATAACTGGATACTGAACTGGATAACTGGAACTGGATACTGAACTGGATACTGAACTGGAACTGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGAACTGGAACTGAACTGGAACTGAACTGGAACTGAACTTAACTGAACTGGAACTGAACTGAACTGAACTGAACTTAACTGAACTGAACTTAACTGAACTGAACTTAACTGAACTGAACTTAACTGAACTGAACTTAACTGAACTTTAACTGAAACTGAAACTTAAACTGAAACTAAACTTTAACTGAAACTGAAACTTAAACTGAAACTTAAACTGAAACTTAAACTGAAACTTAAACTGAAACTTAAACTGAAACTTAAACTGAAACTAAACTAAACTTAAACTGAAACTAAACTTAAACTGAAACTAAACTTAAACTGAAACTAAACTTAAACTTAAACTGAAACTAAACTTAAACTTAAACTGAAACTAAACTAAACTTAAACTAAAACTAAACTAAAAACTAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAAACTAAAAAA
421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAAACTGGACTTTGCCAACTGGATAAAACTGGACTTTGCCAACTGGATAAAACTGGACTTTGCCAACTGGATAAAACTGGACTCGATAATAACTGGACTTTGCCAACTGGATAAAACTGGACTCCCCCGATCCTTAATTTAATCCTCTTAAAAACTGGACTTTTGCCTAATTTTACCCAACTGGAAACTGGACTCAACTGGACTCTAACTTTACCCAATCGATAAACTGGACTCAAACTGGACTCTAACTTTACCCAATCGATAACTGGACTCTAAACTGGACTCTAAACTGGACGAACTGGAAACTGGAAACGGGTGCTTAATTTTCCGCAATCAAACCTTTAACCCATCGGAACTGGAAACGGGTGCTTAATTTTCCGCAATCAAACCTTTAACCCATCGGAACTGGAAACGGGTGCTTAAACTTTCCGCAATCAAACCTTTAACCAACGGAAACCGGTGCTTAAACTTTCCGCAATCAAACCTTTAACCAACGGAAACCGGTGCTTAAACTTTCCGCAATCAAACCTTTAACCAACGGAAACCAACAACCAAACCAAACCAACAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACAAACAAAA
421 TCCAGTCCCGATTCCGTTATTTAATCCTCTAAAACTGGCGTTTGCCAACTGGATAAACTGGCGTTTGCCAACTGGATAAACTGGCGTTTGCCAACTGGATAAACTGGCGTTTGCCAACTGGATAAAACTGGATAAAACTGGATTGCCAACTGGATAAAACTGGATAAAACTGGATTGCCGAACTGAACTGAAACTGGATAAAACTGGATTGCCGAACTGAAACTGGATAAAACTGGATAATTGCTGAACTTTACCGGAACTTAACCGCGAATCAAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTTAACCATCGGAATTAACCAACACATTAACCATCGGAACTGGAAAACAGCATTAACCAACAACAACAACACAACAACAACACAACAAAGCAAAGCAATAAACAGCAACAAACA
421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAAACTGGCTTTGCCAACTGGATAAACTGGCTTTGCCAACTGGATAAACTGGATTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAAACTGGATTAATCCTCTAAAAACTGGCGTTTGCCGAACTGGATAAAACTGGCGTTATTGCTGAACTTGGATAAACTGGCTAATTGCTGAATTGCTGAATCTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAATCAATTGCTGAATTTACCAATCTTACCAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTTAATTTTCCGCAATCAAACTTACCAACTTAACCAACTGAAACTTGAAACTTTACCAACTTTACCAACTTTAACCAACTGAAAACTTGAAACTTTACCAACTTTAACCAACTTTAACCAACTGAAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACTTTAACCAACAA
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The invention discloses a new isolated or recombinant nucleic acid which CC encodes a polypeptide having a phytase activity. Also claimed is a claim nucleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic cacid, a transgenic non-human animal or plant, or its seed, comprising the cardinate of the nucleic acid, an antisense oligonucleotide, inhibiting the polypeptide of a second domain, an array comprising immobilised polypeptide or nucleic acid, a hybridoma comprising an antibody that specifically binds to the polypeptide, a food supplement for an animal, an edible enzyme delivery matrix, an edible pellet comprising a granule edible enzyme delivery colypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, which gain anti-phytase antibody, producing a recombinant polypeptide, determining whether a compound binds to the polypeptide, colippetide, whole cell engineering of new or modified the resistance or thermostability of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a composition and processing of corn and sorghum kernels. The phytase activity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or as an aid in phytate digestion. The sequence presented is the DNA cancerichia coli phytase.
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Best Local Similarity 100.

Matches 1308; Conservative
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improving the feeding value of phytate rich ingredients or as an aid
phytate digestion.
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                                         ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCTA 1308
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ADO50299 standard; DNA; 1308 BP.

29-JUL-2004 (first entry)

Escherichia coli K12 appA phytase mutant 819PH59 DNA

RESULT 2
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XX Esch
XX Esch
XX Esch
XX AppA
XW Phyty
XX Esch
XX Sphyty
XX Sphyt AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; gene; mutant; ds.

Escherichia coli; K12

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TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCCAACTGGATAACGCG 480

421 421

481

AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT

Location/Qualifiers

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ATGAAAGCGATCTTAATCCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA

Query Match Best Local Sim Matches 1308;

Similarity

100.0%;

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Score 1308; Pred. No. 0; 0; Mismatches

BB

12; 0;

Length

Indels

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Gaps

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improve the feeding value of phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially significant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present
                                                                                                                                                                                                                                                          Producing pencoding p
                                                                                                                                     The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast. The inventions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to
Sequence 1308 BP;
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(GRAY/)
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13-APR-1999;
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) BRATON N R.
) GARRETT J B.
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) MATHER E J.
                    is Escherichia coli K12 appA phytase mutant DNA.
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                                                                                                                                                                                                                                                                                                GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA
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                                                                                                                   TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCCACTTCAGTGCTG
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CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC

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The present sequence is that of a polynucleotide encoding a novel modified phytase derived from the Escherichia coli appA protein, with improved thermal tolerance and protease stability compared to the wild-type. The present invention relates to a novel formulation, comprising

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PR 13-AUG-19
PR 13-AUG-19
PR 25-MAY-20
XX (SHOR/) S
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; coding sequence; mutant; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; osteoporosis; osteopathic; food; appA.
                                                                                                                                     Formulation useful as dietary supplement for treating, preventing reversing osteoporosis and bone loss, and preventing muscle cramps comprises one or more polypeptides having phytase activity.
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DB; AEE75421.
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
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99US-00259214.

99US-00291931.

99US-00318528.

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2000US-00866379.
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CC least one polypeptide having phytase activity, where the polypeptide is a CC modified sequence (AEE75421) derived from the Escherichia coli K-12 appA CC phytase (AEE75419). The modification of the enzyme, comprising a series CC of mutations, improves the thermal tolerance and protease stability of CC the protein. The specification also claims a pharmaceutical composition; CC a kit; an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising CC the novel phytase, and a method of reducing pollution and increasing cc nutrient availability in an environment or environmental sample by CC degrading environmental phytic acid. The novel enzyme is a dietary CC supplement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The method is useful for reducing pollution cc and increasing nutrient availability in an environment or environmental cc sample by degrading environmental phytic acid, where the environmental cc environmental sample comprises a soil or a body of water. The immobilized cc phytase is useful in foodstuffs for improving the feeding value of CC phytase is useful in foodstuffs for improving the feeding value of CC phytase is useful in foodstuffs for improving the feeding value of CC phytate rich ingredients.
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/EC number= "3.1.3.8"
/partial
/product= "Escherichia c
/note= "No stop codon"
                                                                                                                                                              ocation/Qualifiers
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Matches 1296;
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also useful in gene therapy and in production of transgenic animals. The present sequence is the SEQ ID NO: 1 which is given in the sequence listing. This sequence differs from the SEQ ID NO: 1 shown on page 19 in disclosure of the specification (see AED50824).
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Mathur EJ;
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(KRET/)
(GRAY/)
(BART/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) ODONOGHUE E.
) MATHUR E J.
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                                                                                                                                                                                        ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA
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                           GCCTTCGCCGGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                                                                      CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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99US-00291931.

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2001US-00866379.

2002US-00156660.
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                           CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTTACGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGACATTACCCCACTTCAGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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                                    appA phytase
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                                      DNA sequence SEQ
protein stabilization;
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660

720

600 600 540 540 480

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osteopathic; food; appA.
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                                           /note= "Wild type !
replace(864,A)
/*tag= t
                                                                                                                                                                                                                                                     /note= "Wild type replace(476,A)
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/note= "Wild type
replace(470,G)
                                                                replace(863,A)
/*tag= s
                                                                                         /note= "Wild type
replace(730,G)
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replace(729,G)
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replace (728, C)
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replace(691,C)
                                                                                                                                                                        replace (690,G)
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replace(477,A)
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                               /note= "Wild type
replace(1016,T)
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replace(437,C)
                                                                            note= "Wild type
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                                                                                                                                                                                                                                                                                                                                         note= "Wild type base C replaced
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TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT

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247

TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT

ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTTCTGATTCCGTTAACCCCGCAATCTGCA

ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA

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Matches

1296;

Conservative

0

Mismatches

4. 15;

Indels

Gaps

Query Match Best Local Similarity

98.9**%;** 99.7**%**;

Score 1294.2; Pred. No. 0;

Sequence

1901

BP;

470 A; 497 C; 500 G; 433

H, 멂

0 U;

1 Other, Length

1901; 0,

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The present sequence is that of a polynucleotide encoding a novel compodified phytase derived from the Escherichia coli appA protein, with compoditive proved thermal tolerance and protease stability compared to the wild-cipe. The present invention relates to a novel formulation, comprising at compodified sequence (AEE75419) are compodified from the Escherichia coli K-12 appA compodified sequence (AEE75419). The modification of the enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition; a kit, an immobilized phytase; a fertilizer or soil additive; a liquid colluture or cell culture media; and a plant food additive, all comprising nutrient availability in an environment or environmental sample by degrading environmental phytic acid. The novel enzyme is a dietary complement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful campis. The method is useful for reducing pollution and increasing nutrient availability in an environment or envi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Formulation useful as dietary supplement for treating, preventing reversing osteoporosis and bone loss, and preventing muscle crampu comprises one or more polypeptides having phytase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 82pp; English.
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(KRET/)
(GRAY/)
(BART/)
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
BAUM W.
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                        CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                                                                                                                              ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGGTGAACTGGTGTTTGAACGCTGG
                                                                                                                                                                                                                                                                                                                    TTGACGCCCCATCCACCGCAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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                                                                                                                            (GARR/)
(ODON/)
(MATH/)
                                                                                                                                             (SHOR/)
(KRET/)
(GRAY/)
(BART/)
                                                                                                                                                                                                                    20-JUN-2003;
                                                                                                                                                                                                                                            US2004091968-A1.
                                                                                                                                                                                                                                                              mutation
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) O'DONOGHUE I
) MATHER E J.
                                                                                                           ЕJ;
                                                                                                                                             SHORT J M.
KRETZ K.
GRAY K A.
BARTON N R.
                                                                                                                                                                                                                                                                                                                        animal feed;
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                                                                                                                                                                                                                                                                                                                                                                             standard;
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99US-00259214.

99US-00291931.

99US-00318528.

2000US-00580515.

2001US-00866379.
                                                                                                                                                                                                                                                                                                                                         coli K12 appA phytase mutant
                                                                                                                                                                                                                                                                                                             coli;
                                                                                                                                                                                                                    2003US-00601319
                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                              bacteria; thermal tolerance; protease stability; foodstuff;
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replace(439,A)
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Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid 2004-374952/35

SEQ ID NO 6; 74pp; English

The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially

문 S

CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260

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Matches 1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1901 BP; 472 A; 498 C; 501 G; 429 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is Escherichia coli K12 appA phytase mutant DNA.
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       CGCACGCCAGAGGTTGCCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
                                   CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG
                                                                                            GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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Escherichia
                                                                                            Escherichia coli K12 appA phytase mutant DNA
                                     AppA phytase; phytate; anima
                                                                                                                                     29-JUL-2004
                                       tase; bacteria; thermal tolerance; proto
animal feed; fish feed; dough; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT
                                                                                                                                                                                                                                                                                                         ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
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                                                                                                                                                                                                                                                                                                                                                                                  CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA
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 <u>K1</u>2
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                                                  protease stability;
                                                                                              #1.
                                       gene;
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                                         mutant;
                                                          foodstuff;
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13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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SHORT J M.
KRETZ K.
GARTON N R.
GARRETT J B.
O'DONOGHUE E.
MATHER E J.
                                                                                                   99US-00318528
2000US-00580515
2001US-00866379
                                                                                                                                                                                         2003US-00601319
                                                                                                                                        97US-00910798.
99US-00259214.
99US-00291931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Short JM,
Mather EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1901 BP;
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               TATCAAACGGCGTTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
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                                                                                                                                         TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                                                                                                                                                                                           GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
                                                           AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                              AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                                     TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                                                                                                                                                                                                                          CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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98.4%;
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Pred. No. 0;
0; Mismatches
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13-AUG-1997;
01-MAR-1999;
                                           01-SEP-2004; 2004US-00933115
                                                                         22-DEC-2005
                                                                                                                                    Escherichia
                                                                                                                                                                fertilizer;
                                                                                                                                                                                                                                          23-FEB-2006
                                                                                                                                                                                                                                                                                                    AEE75416 standard;
                                                                                                                                                                                                           coli phytase related DNA sequence
                                                                                                                                                                             thermostable; phytase; protein stabilization; pharmaceutical;
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97US-00910798
99US-00259214
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                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a DNA sequence related to the production of the covel thermostable / protease resistant Escherichia coli phytase CC described in the specification. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, CC where the polypeptide is a modified sequence (AEB7542) derived from the Escherichia coli K-12 appA phytase (AEB75419). The modification of the CC enzyme, comprising a series of mutations, improves the thermal tolerance CC and protease stability of the protein. The specification also claims a CC pharmaceutical composition; a kit; an immobilized phytase, a fertilizer or soil additive, a liquid supplement for preventing muscle cramps; a CC hydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing pollution and increasing nutrient availability in an environment or environmental sample by degrading environmental phytic acid. The novel carding supplement is useful for treating preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The method is useful for reducing pollution and increasing mutrient availability in an environment or environmental sample by degrading environmental phytic acid, where the environmental sample by degrading environmental phytic acid, where the environmental sample by degrading environmental phytic acid, where the environmental or environmental sample comprises a soil or a lody of water. The immobilized phytase is useful in foodstuffs for comprise a soil or a lody of water. The immobilized phytase is useful in foodstuffs for The CC present sequence is shown in the sequence listing but not discussed a sole or alsowhere in the servicion of the sequence is shown in the sequence of 
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1279; Conser
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25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                 Sequence 1901 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         phytase enzym
the phytates.
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                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                   Improving the nutritional value of phytase enzymes which catalyze the
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                                                                            GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG
                                                                                               ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGGTGAGCTAATCGCCTATCTC
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                           CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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                                                                                                        ACCTGGCCGGTAAAACTGGGTGAGCTGACCACCGCGGTGGTGAGCTAATCGCCTATCTC
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AAD36473 standard; DNA; 1323 ВÞ

21-AUG-2002 (first entry)

Escherichia coli phytase DNA

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1323
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                     ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC
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                                                                                                                                                                                                                                                                                                                                                                       TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTTACCCACTTCAGTGCTG
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    ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC
                                                                                 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                                    CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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RESULT 12
ADA19445
The invention relates to an isolated Escherichia coli polynucleotide CC encoding a phytase enzyme appearing as ADA19450 and having amino acids CC modification from W68E, O84W, A95P, K97C, S168E, R180Y, R926C or Y277D. CC Also included the E. coli appA gene ADA1949 (or an oligonucleotide CC derived from it) or its mutant sequence ADA19452, expression vectors, host cells, a method of improving nutritional value of a phytate-CC containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in the phytate-CC containing foodstuff), a method to produce an animal feed containing a CC microbial phytase (comprising culturing the plant cell, plant part or plant under conditions where the nuclectide sequence is expressed and CC converting the plant cells, plants or plant into a composition for animal (cells, plant parts or plants in admixture with a phytate-containing foodstuff), a method to treat a human or an animal able to benefit from CC digestive enhancement by the activity of an exogenous phytase enzymes comprising administering to the human or animal the plant seed, plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000; 2
                                                                                                                                                                                                                                                                                                Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                 Short JM, 1
O' Donoghue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GRAY/)
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) KRETZ K A.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O' DONOGHUE
) MATHUR E J.
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; 99US-00259214.
; 99US-00291931.
; 99US-00318528.
; 2000US-00580515.
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/product= "Phytase"
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TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC

AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT

AACGTGACTGACGCGATCCTCAGCAGGGGCAGGGAGGGTCAATTGCTGACTTTACCGGGCAT

TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG

TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG

GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG

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GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG

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CGGCAAACGGCG

CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC

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721 781

GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA

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GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA

AAGGTGAGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGAACGGGAGATATTTCTCCTGCAACAAGGACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC

GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence encoding a phytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a polypeptide having phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence encodes E. coli B wild-type phytase.
                                                                                                                                                                                                                                                                                                                                                              Sequence 1323
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                            ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGCGTGGTGAGCTAATCGCCTATCTC
                                                                     GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
                                                                                                       GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC
                                                                                                                                          TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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                                                                                                                                                                                                                                                                                       Conservative
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98.0%;
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
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24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unsure
  (KRET/)
(GRAY/)
(BART/)
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                                                                                                                                                                                                                                                                                                    20-JUN-2003;
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  SHORT J M.
KRETZ K.
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BARTON N R.
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The invention relates to a method for producing phytase that involves corporating a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow compression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of commercous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, composition, higher yields and loading efficiency. The phytase composition, higher yields and loading efficiency. The phytase concorporated in to the dietary aid is safe for animals. The present composition is Escherichia coli B phytase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Short JM,
Mather EJ;
                                                                                                                                                                                                                                                                                                                                            Producing phytase, in encoding polypeptide
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P-PSDB; ADOS0292.
                                                                                                                                                                                                                                                                                                  Claim 3;
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(ODON/) O'DONOGHUE
(MATH/) MATHER E J.
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SQ Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;

Query Match 96.7%; Score 1265; DB 12; Length 1323;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTGATTCCGTTAACCCCGCAATCTGCA

Query Match Best Local Sim Matches 1280;

Similarity

96.7%; llarity 98.0%; Conservative

Score 1265; I Pred. No. 0; 0; Mismatches

DB

12; 26;

Indels Length 1323; 1 Other;

0

Gaps

0

Sequence 1323

BP; 325 A; 353

ç;

356 G; 288 T; 0 U;

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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Kangaroo rat Escherichia coli phytase mutant DNA. Note: The present sequence is not shown in the specification but has been derived from Escherichia coli B phytase DNA ADOS0291.
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25-MAY-2000;
24-MAY-2001;
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Mather EJ;
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(KRET/)
(GRAY/)
(BART/)
(GARR/)
(ODON/)
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                                                                                                                                                                                                                                                                                                                                  Producing phytase, involves encoding polypeptide having
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E
) MATHER E J.
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replace(893,T)
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                                                                       ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCTGG
                                                                                                                                                  TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG

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Producing phytase, involves providing nucleic acid derived

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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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Mather EJ;
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(ODON/)
(MATH/)
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(KRET/)
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P-PSDB; ADO50292, ADO50304.
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                                                                                                                                                         ) SHORT J M.
) KRETZ K.
) GRAY K.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease ctability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve that including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant mammals such as sigs, goats, laboratory rodents, commercially CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in distary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present sequence is scherichia coli M phytase mutant DNA. Note: The present concerned is shown in the specification but has been derived from Excherichia coli B phytase DNA ADOS0291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1280;
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CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                                             TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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Search completed: June 14, 2006, 10:31:29 Job time : 893.897 secs

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4	181 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGCGGTGGTGAGCTAATCGCCTATCT	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCC.	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT	1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTC	Match 96.7%; Score 1265; DB 2; Local Similarity 98.0%; Pred. No. 0; Local Similarity 08.0%; Pred. No. 0;	T 1 133 AR108133 1323 bp DNA ITTON Sequence 1 from patent US 6110719. SION AR108133 ON AR108133.1 GI:12823620 RDS Unknown. B Unknown. LOCALESTIED. ANISM Unclassified. ENCE 1 (bases 1 to 1323) HORS Kretz,K. LB Phytase RNAL Patent: US 6110719-A 1 29-AUG-2000; RES LOCALION/Qualifiers RES 1. 1323 //mol_type="unknown" /mol_type="unknown"	ALIGNMENTS	1262.2 96.5 1901 2 AX356570 1262.2 96.5 1901 2 AX356574 1262.2 96.5 1901 15 ECOACPHB 1261.6 96.5 1315 15 AF537219 1260.6 96.4 1901 15 ECOACPHE 1260.6 96.4 1901 15 ECOACPHE 1260.6 96.4 1901 15 ECOACPHE 1259.2 96.3 3470 2 AX042374 1259.2 96.3 6116 2 AX042375 1259.2 96.3 6708 2 AX042373 1259.2 96.3 17732 2 AX042373 1259.2 96.3 1901 15 ECOACPHA 1259.2 96.3 1901 15 ECOACPHA 1259.2 96.3 12732 2 AX042372 1259.2 96.3 12732 2 AX042373 1259.2 96.3 1901 15 ECOACPHA 1259.2 96.3 1901 15 ECOACPHA 1259.3 96.3 1901 15 ECOACPHA 1259.3 96.3 1901 15 ECOACPHA 1259.4 95.3 10000 15 AE005674 10 1237.6 94.6 110000 15 AE00573 10 1238.8 93.9 1489 2 AR277753 1228.8 93.9 1489 2 AR277753 1218.8 93.2 110000 15 AE005174 12	
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B 1 (bases 1 to 1323)

S Short, J.M. and Kretz, K.A.

Recombinant bacterial phytases and use Patent: US 6183740-A 1 06-FEB-2001;
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GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	ATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	Query Match Best Local Similarity 98.0%; Pred. No. 0; Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	rce 11323 /organism="unknown" /mol_type="unassigned DNA"	Kretz,K. Phytase Patent:	3	V Sequence 1 from patent US 6190897. AR130956 AR130956.1 GI:14119281	AR130956	1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC 1306	1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGGCCG	1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	961 TITATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020 	901 TIGACGCCCCAICCACCGCAAAAACAGGCGTAIGGTGTGACATTACCCACTTCAGIGCIG 960 	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGAC	781 GATTCACACAGTGGAACACCTTGCTAAGTTTGCATAAGGCGCAATTTGATTTGCTACAA 840	GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC
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Matches 1280; Conservative
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Patent: US 6720014-A 1 13-APR-2004;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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Short, J.M. and Kretz, K.A.
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                                                 TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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Short,J.M., Kretz,K.A., Gray,K.A., Ba Short,J.M., Kretz,K.A., Gray,K.A., Ba O'Donoghue,B. and Mathur,E.J.
Recombinant bacterial phytases and us Recombinant bacterial phytases and us Patent: US 685365-A 1 15-FEB-2005; Patent: US 685365-A 1 15-FEB-2005; Diversa Corporation; San Diego, CA Location/Qualifiers
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                                                   Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria;
Bacteria; Proteobacteria; Gammaproteobacteria;
O'Donoghue, E.
Recombinant bacterial phytases and uses
Patent: WO 0190333-A 1 29-NOV-2001;
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Sequence 1 from Patent WO0190333.
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                 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                                                                              CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                                               TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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                                                              CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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PPGGVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSLRSHHHHHHH"
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RESULT 9
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AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720
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Query Match Best Local Similarity	Continuation (11 of 47)	U00096_46		U00096_44		U00096_42	U00096_41	U00096_40	U00096_39		U00096_37			U00096_34		U00096_32				U00096_28		U00096 26
96.7%; 98.3%;	of U0009	4600001	4500001	4400001	4300001	4200001	4100001	4000001	3900001	3800001	3700001	3600001	3500001	3400001	3300001	3200001	3100001	3000001	2900001	2800001	2700001	2600001
Score 1264.8; Pred. No. 0;	6 from base 1000001 (U00	4639675	4610000	4510000	4410000	4310000	4210000	4110000	4010000	3910000	3810000	3710000	3610000	3510000	3410000	3310000	3210000	3110000	3010000	2910000	2810000	2710000
DB 15; Length 110000;	Continuation (11 of 47) of U00096 from base 1000001 (U00096 Escherichia coli K-12 MGL655																					

1 AT	ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	0
39840 AT	39840 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 39899	9899
61 TT	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	20
39900 TT	39900 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 39959	9959
121 GI	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	80
39960 GI	39960 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 40019	0019
181 AC	181 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGCGC	40

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40020	ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCCGGTGGTGAGCTAATCGCCCTATCTC	40079
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301		360
40140	CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGGGTAAAACAGGCGAA 4	40199
361		420
40200	GCCTTCGCCGGCCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG 4	40259
421	TCCAGTCCCGATCCGTTATTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 4	480
40260		40319
481		540
40320	AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 4	40379
541		600
40380	CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC	40439
601	CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	60

RESULT 10 APRO09048_10 WPCCMMENT Sequence split into 47 fragments LOCUS APRO09048 Accession APR009048 Fragment Name Begin End APRO09048_00 1 100001 210000 APRO09048_01 100001 310000 APRO09048_02 200001 310000 APRO09048_03 300001 410000 APRO09048_05 500001 510000 APRO09048_06 600001 710000 APRO09048_08 800001 1010000 APRO09048_09 900001 1010000 APRO09048_10 1000001 1100000 APRO09048_11 11000001 1100000 APRO09048_12 1200001 1310000 APRO09048_13 1300001 1310000 APRO09048_13 1300001 1510000 APRO09048_14 1400001 1510000 APRO09048_15 1500001 1510000 APRO09048_16 1600001 1710000 APRO09048_17 1700001 1810000 APRO09048_18 1 1800001 1710000 APRO09048_19 1900001 1910000 APRO09048_19 1900001 1910000 APRO09048_19 1900001 2210000 APRO09048_20 2000001 2310000 APRO09048_21 2100001 2310000 APRO09048_22 2200001 2310000 APRO09048_23 2300001 2510000	AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTC 721 GAGATATTTCTCCTTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGAGGAACGATC 721 GATTCACACCAGTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGAGGAACGATC 721 GATTCACACCAGTGCAACAAGCACCGTTGCTAAGTTTGCATAACGCGCAATTTGATTTGATTTGCTT 722 GATTCACACCAGTGGAACACCCTTGCTAAGTTTGCATAACGCGCAATTTTGATTTATTT
Qy 241 GGACATTACTGGCGTAAACTGGTTGGTTAGCCGACGGATTGCTCATATCGCCTAATTGCCCG 41278 Qy 241 GGACATTACTGGCGTCAGCGTCTGGTTAGCCGACGGATTGCTGCCTAATTGTGCCCG 300	AP009948 25 250001 2510000 AP009948 26 260001 2710000 AP009948 27 2700001 2710000 AP009948 28 2800001 2710000 AP009948 28 2800001 2710000 AP009948 29 2800001 3710000 AP009948 29 2800001 4710000 AP009948 20 280001 4710000 AP009948 20 2800001 4710000 AP009948 20 280001 4710000 AP009948 20 280001 4

Alifiers Inknown Jenomic DNA Jenomic DNA Score 1263 Score 1263 Pred. No. O; Mismatc SOURCE Unknown. SOURCE Unknown. ORGANISM Unknown. Unclassified. Unclassified. Viclassified. I (bases 1 to 1901) AUTHORS Short, J.M., Kretz, K.A., Gray, K.A., Barton, N.R., Garrett, J.B., O'Donoghue, E. and Mathur, E.J. TITLE Recombinant bacterial phytases and uses thereof JOURNAL Patent: US 6855365-A 6 15-FEB-2005; Diversa Corporation; San Diego, CA	RESULT 11 AR636189 LOCUS AR636189 DEFINITION Sequence 6 from patent US 6855365. ACCESSION AR636189 VERSION AR636189.1 GI:62768872	Oy 1201 CTGGCAGGATGTGAACAGCCAAATGCGCAAGGCCATGGTTGTTGCCAGA 1260	Qy 1081 CGTCGGCTTAGCGATTACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG 1140 Db	961 41999 1021 42059	OY 841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCGCCCCCTTATTAGATTTGATCAAGACAGCG 900	Db 41699 AAGGTGAGCGCGACAATGTCTCATTAACCCGGTGCGGTAAGCCTCGCATCAATGCTGACG 41758 Qy 721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGGAAGGATCACC 780	
961 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG	Db 968 GATTCACACCAGGGGAACACCTTGCATAACGGGGCAATTTTATTTTGCTACAA 1027 Qy 841 CGCACGCCAGAGGTTGCCCGCAGCCACCCCGTTATTAGATTAGACAACAGCG 900	Db 848 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACC 907 Qy 721 GAGATATTTCTCCTCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780	Db 728 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 787 Qy 601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	Db 608 TCCAGTCCCGATCCGTTATTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 667 Qy 481 AACGTGACCTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACCTTTACCGGGCAT 540	CAGTCTGGTCAGGTCAGCATTATTGTCTGTGTCAACGAGCGTACACCAGGCAAAACAGGCGAA GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACC [Db 368 ACCTGGCGTAAAACTGGGTTGGTTGACACCGCGGGGTGGTGAATGCCCTATCTC 427 Qy 241 GGACATTACTGGGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG 300	Oy 61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120

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Short, J.M., Kretz, K.A., Gray, K.A., Barton, O'Donoghue, B. and Mathur, B.J.
Recombinant bacterial phytases and uses th Patent: US 6855365-A 7 15-FEB-2005;
Diversa Corporation; San Diego, CA Location/Qualifiers
ce 1. 1901
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                                          TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCG
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Sequence 6 i
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/mol_type="unassigned DNA"
/db_xref="taxon:562"
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Pred. No. 0;
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Best Local Similarity
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Sequence
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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                                                           ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGGGGTGGTGAGCTAATCGCCTATCTC
                                                                                            GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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/mol_type="unassigned I
/db_xref="taxon:562"
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Patent WO0190333.
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The complete nuclectide sequence of the reveals significant homology between pH glucose-1-phosphatase
J. Bacteriol. 172 (9), 5497-5500 (1990)
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Asp304 of Escherichia coli acid phosphatase
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              PPGEVKLTLAĞCEERNAQGMCSLAGFTQIVNBARIPACSL
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Job time : 7319.05 secs	428 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 487	밁
Search completed: June 14, 20	241 GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG 300	Ś
DD 1440 AICGIGMAIGMAGCA	368 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 427	밁
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	181 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGCGGTGGTGAGCTAATCGCCTATCTC 240	8
1261	308 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 367	밁
Db 1388 CTGGCAGGATGTGAA	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	8
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Db 1328 CAGATGCGTGATAAA	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	ş
11/1	188 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 247	뭥
	1 ATGAAAGCGATCTTAATCCCCATTTTTATCTCTTCTGATTCCGTTAACCCCCGCAATCTGCA 60	ş
1208	Hest Local Similarity 98.2%; Fred. No. 0; Mismatches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;	3 12
1021		۵
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/BE_COMB.seq:*
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                1403666 seqs, 935554401 residues
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US-09-715-798-3515
US-09-902-540-3515
US-09-902-540-3168
                                 US-09-103-840A-2
US-09-103-840A-1
US-09-103-840A-2
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Sequence 16384, A	Sequence 3/32, Ap		Sequence 94, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 1286, Ap	Sequence 3, Appli	Sequence 16326, A	Sequence 14187, A	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 116, App	Sequence 1, Appli	Sequence 8976, Ap	Seguence 14757, A	Sequence 5, Appli	Sequence 109217,	Sequence 109216,	Sequence 109215,

ALIGNMENTS

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; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; PEATURE:
; NAMB/KEY: CDS
; LOCATION: (1)...(1320)
; NAMB/KEY: misc feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or
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Patent No. 6110719
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REBERENCE: DIVERIJO-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity
Matches 1280; Conserv
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                    ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGGTGGTGAGCTAATCGCCTATCTC
                                                                                     GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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; Sequence 1, Application U
; Patent No. 6183740
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
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FILE REPERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
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; LOCATION: (1)...(1323)
; OTHER INFORMATION: n =
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FEATURE:
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               TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                             AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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GENERAL INFORMATION:
APPLICANT: Kretz, Keith
ITITLE OF INVENTION: NOVEL PHYTASE
ITITLE OF INVENTION: NOVEL PHYTASE
ITITLE OF INVENTION: NOVEL PHYTASE
ITITLE OF INVENTION: 1990-03
CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1990-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
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; Patent No. 6190897
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FILE REFERENCE: DIVERLIGION:
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
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Patent No. 6855365
GENERAL INFORMATION:
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Best Local Similarity 98.0%;
Matches 1280; Conservative
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APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Elleen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
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                                                                                GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG
                                                                                                        GGACATTACTGGCGTCAGCGTAGCCGACGGATTGCTGCCCTAAATGTGGCCTGCCCG
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Pred. No. 0;
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RESULT 6
US-09-866-379-6
US-09-866-379-6;
Sequence 6, Application US/098663;
Patent No. 6855365;
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
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SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 1901

TYPE: DNA

ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1). - (1901)

OTHER INFORMATION: n is any nucleotide
US-09-866-379-6
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APPLICANT: BARTON, Nelson
APPLICANT: DARRETT, James
APPLICANT: O'DONOCHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/886,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
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                 TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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Pred. No. 0;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James

US-09-866-379-7

Sequence 7, Application US/09866379 Patent No. 6855365

APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214

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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n is any nucleotide
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PRIOR APPLICATION NUMBER: US 0.
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
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Best Local Similarity 98.2
Matches 1277; Conservative
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GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA
                                                        GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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Sequence 5, Application US/09866379
Patent No. 6855365
GENERAL INFORMATION:
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 09/259,214
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                                   TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
                                                                                   TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
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ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
                                                                                                                       CGCACGCCAGAGGTTGCCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR PELLING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR TILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
                                                                                                                                                                                                                                                                                               ORGANISM: Escherichia coli;
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (1901)
OTHER INFORMATION: n is any nucleotide
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US-09-866-379-9
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Best Local S
Matches 1276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
FILE REFERENCE: DIVER1370-7
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TYPE: DNA
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                     GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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                CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260
                                                                                 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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; Sequence 2, Application US/09715477
; Patent NO. 6841370
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
; FILE REFERENCE: 19603/4031
; CURRENT APPLICATION NUMBER: US/09/715,477
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,179
; PRIOR APPLICATION NUMBER: 09/11-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1486
; TYPE: DAN
; ORGANISM: Escherichia coli
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               CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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                                                                                 TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                             AACGTGACTGACGCGATCCTCAGCAGGGGCAGGGGGTCAATTGCTGACTTTACCGGGCAT
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CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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nilarity 97.0%;
Conservative
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1202 ACGCTTCCAGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTG 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTC	δ B	Best Local Similarity 96.5%; Pred. No. 0; Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps 1 ATGABAGGGATGTTABATGGGATGTTTABTGGGATGTGGATTGGGATGGGATGTGGATGGGATGTGGATGGGATGGGATGTGGATGGGATGTGGATGGGATGTGGATGGATGGATGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGATGGGATGGGATGGGATGGGATGGATGGATGGGATGAT
	. Q	93.98;
961 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACTGG	ድ	; SEC 1D NO 9 ; LENGTH: 1489 ; TYPE: DNA ; ORGANISM: Escherichia coli
901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG	A5 48	PRIOR FIL NUMBER OF SOFTWARE:
841 CGCACGCCAGAGGTTGCCCGCGAGCCGCGCGACCCCGTTATTAGATTTGATCAAGACAGCG	₽ Q	FILE REFERENCE: 19603/2791 CURRENT APPLICATION NUMBER: US/09/540,149A CURRENT FILING DATE: 2000-03-31 DETOR APPLICATION NUMBER: 05/127 032
781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA 	gg Qg	DBOMBD DUVENCE
721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC	g Qy	RESULT 11 US-09-540-149A-9
661 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG	g Qy	Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1296
601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC	B &	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260
541 TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC	B &	Qy 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC 1200
481 AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT	g 84	Qy 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140
421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG	gg Qy	Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080
361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG	B 8	QY 961 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGGCG
301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 	g Q	Qy 901 TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 960
241 GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG	B &	Qy 841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG 900
181 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGGGTGGTGAGCTAATCGCCTATCTC	B &	Qy 781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA 840
121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA	B &	Qy 721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780
61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT	Qy Db	Qy 661 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720

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APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVED PHYTASE ACT.
FILE REFERENCE: 19603/2798
CURRENT APPLICATION NUMBER: US/10/266,041A
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEG ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
SEG ID NO 9
LENGTH: 1489
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Best Local Similarity 96.5%;
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AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540
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Pred. No. 0;
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                                                                              GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
FILE REFERENCE: 19603/4031
CURRENT FILING DATE: 2000-11-17
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION UNMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-18
INUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-715-477-4
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Query Match 93.5
Best Local Similarity 96.5
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                                                                                                                                     Sequence 1, Application Patent No. 5876997
                                                    Matches 1229;
                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D.; LISA:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KRETZ
TITLE OF INVENTION: NOVEL PHYTASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suit
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRESENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                   NAME/KEY:
LOCATION:
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ZIP: 92037
                                                   Local Similarity 94.1
es 1229; Conservative
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                                                 Score 1153;
Pred. No. 0;
0; Mismatches
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; Sequence 341, Application US/09489039A
; Patent No. 6610836
; Patent No. 6610836
; GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KITILE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FALING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 341
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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ALIGNMENTS

Sequence 2, Application US/09777566A Patent No. US20010055788A1 GENERAL INFORMATION: APPLICANT: DIVERSA CORPORATION APPLICANT: SHORT, Jay APPLICANT: SHORT, Jay APPLICANT: SHORT, Jay APPLICANT: SHORT, Jay APPLICANT: RECOMBINANT BACTERIAL PHYTASES AND FILE REFERENCE: DIVER1370-6 CURRENT APPLICATION NUMBER: US/09/777,566A CURRENT FILLING DATE: 2001-06-11 PRIOR APPLICATION NUMBER: US 09/318,528 PRIOR APPLICATION NUMBER: US 09/291,931 PRIOR APPLICATION NUMBER: US 08/910,798 PRIOR PILLING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: US 08/910,798 PRIOR PILLING DATE: 1997-08-13 NUMBER OF SEQ ID NOS: 4 CONTEMBER OF SEQ ID NOS: 4 ; LENGTH: 440 ; TYPE: PRT ; ORGANISM: Escherichia coli ; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (1)...(1323) ; OTHER INFORMATION: n is any nucleotide US-09-777-566A-2 US-09-777-566A-2 'SOFTWARE: PatentIn version 3.0 SEQ ID NO 2 Query Match Match 100.0%; Local Similarity 100.0%; les 440; Conservative 0 Score 2302; DB 3; Pred. No. 2.2e-193; 0; Mismatches 0; AND Length 440; USES THEREOF

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181 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT

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61 TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120 1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP

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Matches 440;

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Gaps

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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLB OF INVEXTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1000-05-25
PRIOR FILING DATE: 199-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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TYPE: PRT
; ORGANISM: Escherichia coli
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Matches 440; Conserv
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                       RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
                                                                                                          AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
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APPLICANT: K-etz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION UNMERR: US/10/034,985
CURRENT APPLICATION UNMERR: US/9580,515
PRIOR APPLICATION UNMERR: US/9580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION UNMERR: 09/291,931
PRIOR APPLICATION UNMERR: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR PRIOR PRIOR DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-13
PRIOR PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
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Publication No. US20030049815A1
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Best Local
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RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPBGEVKLTLAGCEERNAQGMCSLAGFTQ
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APPLICANT: Kretz, Keith
FILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/02903
CURRENT APPLICATION NUMBER: US/10/430,356
CURRENT APPLICATION NUMBER: US/9/580,515
PRIOR APPLICATION NUMBER: US/9/580,515
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 09/292,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
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US-10-430-356-2
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Best Local Similarity
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                               IVNEARIPACSLRSHHHHHH 440
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Pred. No. 2.2e-193;
Mismatches 0; Indels 0
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APPLICANT: Garrett, James B.
APPLICANT: OD DONOSHUE, Eileen
APPLICANT: O' DONOSHUE, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND MET
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR PPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/290,931
PRIOR APPLICATION NUMBER: US 09/290,931
PRIOR APPLICATION NUMBER: US 09/290,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
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Best Local Similarity 100.0%;
Matches 440; Conservative 0
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
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ORGANISM: Escherichia
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                                                                                                                RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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I VNEAR I PACSLRSHHHHHH
                        IVNEARIPACSLRSHHHHHH 440
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                                                                                RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 2.2e-193;
0; Mismatches 0;
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US-10-933-115-2

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; Sequence 2, Application US/10933115
; Publication No. US20050281792A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Kretz, Keith A.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Garrett, Nelson Robert
; APPLICANT: Garrett, James B.
; APPLICANT: Gorrett, James B.
; APPLICANT: O' Donoghue, Eileen
; APPLICANT: Mathur, Eric J.
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 564462001822
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; LENOTH: 440
; TYPE: PRT
; ORGANISM: Escherichia c
US-10-933-115-2
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CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-03-01
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Best Local
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440; Conser
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                                   IVNEARIPACSLRSHHHHHH 440
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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USE
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Vay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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US-09-866-379-8
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Best Local Similarity
Matches 430; Conserv
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    IVNEARIPACSL 432
                                                 RRISDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 1.7e-187;
0; Mismatches 2;
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421

US-10-156-660-4

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FILE REFERENCE: 09010-029007

CURRENT APPLICATION NUMBER: US/10/156,660
CURRENT FILING.DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FABRISEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 432
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Publication No. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
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APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS
TITLE OF INVENTION: AND METHODS FOR MAKING
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IVNEARIPACSL 432
                          IVNEARIPACSL 432
                                                                         RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                    RRLSDNSQWIQVSLVPQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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99.5%;
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APPLICANT: ADMINISTRY, R.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Gen
FILE REFERENCE: ELITERA.034A

CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: G0/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/247,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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US-10-282-122A-43351
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US-10-282-122A-43351
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SEQ ID NO 43351
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Mando, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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APPLICANT:
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Local Similarity 99.5%;
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                                             EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300
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EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Pred. No. 1.7e-187;
0; Mismatches 2; Indels
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PRIOR FILLING DATE: 2001-05-24
PRIOR PELLICATION NUMBER: US 09/580,515
PRIOR FILLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILLING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
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                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 8
LENGTH: 432
TYPE: PRT
ORGANISM: Escherichia
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PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FastSEQ for Windows Version 4
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APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
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No. US20040091968A1
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                                                            RQTAFRELERVINFPQSNICCIKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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Gray, Kevin A.
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APPLICANT: Cargill, Incorporated
TITLE OF INVENTION: Myo-Inositol Oxygenases
FILE REFERENCE: 10829/003US1
CURRENT APPLICATION NUMBER: US/10/472,317
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/US02/08404
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR PILING DATE: 2001-03-19
INUMBER OF SEQ ID NOS: 72
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
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US-10-472-317-41
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Best Local Similarity
Matches 430; Conser
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                                 IVNEARIPACSL 432
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Pred. No. 1.7e-187;
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PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR RILING DATE: 1999-05-25
PRIOR RILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER: OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 432
TYPE: PRT
ORGANISM: Escherichia coli
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US-10-933-115-8
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Best Local Similarity 99.5
Matches 430; Conservative
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Publication No. US20050281792A1
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TITLE OF INVENTION: RECOMBLINANT BACTERIAL
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT FILING DATE: 2004-09-01
CURRENT FILING DATE: 2004-09-01
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
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Garrett, James B.
O' Donoghue, Eileen
Mathur, Eric J.
                            IVNEARIPACSL 432
                                                                                                                       LTPHPPQKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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APPLICANY: OPANCE:
APPLICANY: O'DONCGHUE, Elieen
APPLICANY: O'DONCGHUE, Elieen
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM AND METHODS
TITLE OF INVENTION: POR MAKING AND USING THEM
FILE REFERENCE: 564462001803/D1370-9C1
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 10/156,660
PRIOR PRIOR PHILING DATE: 2002-05-24
PRIOR PHILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-08-01
PRIOR PILING DATE: 1999-08-01
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Publication No. US20050246780A1
GENERAL INFORMATION:
APPLICANT: SHORT, Jay M.
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Nelson R.
APPLICANT: GARRETT, James B.
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; ORGANISM: Escherichia coli appA phytase
US-11-056-354-4
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SOFTWARE: PatentIn version
SEQ ID NO 4
LENGTH: 432
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Local Similarity 99.5%;
les 430; Conservative
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                        RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420
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Pred. No. 1.7e-187;
0; Mismatches 2;
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APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/11/018,709
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: US/09/715,477
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARR: Patentin Ver. 2.1
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US-10-284-962-3
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; LENGTH: 432
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-018-709-1
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US-11-018-709-1
Sequence 3, Application US/10284962
Publication No. US20030206913A1
GENERAL INFORMATION:
APPLICANT: Webel, Douglas M.
APPLICANT: Orr, Donald B.
APPLICANT: Ruch, Frank B.
APPLICANT: Ruch, Frank B.
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Similarity 99.3%;
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Pred. No. 4.6e-187;
0; Mismatches 3;
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US-10-284-962-3
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LENGTH: 432
TYPE: PRT
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Best Local Similarity 99.1%;
Matches 428; Conservative
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CURRENT APPLICATION NUMBER: US/10/284,962
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/335,303
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
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pred. No. 2.8e-186;
0; Mismatches 4;
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Search completed: June 13, Job time : 145.303 secs 2006, 10:50:37

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RB_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RB_COMB.pep:*
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US-09-540-149A-1
US-10-266-041A-1
US-09-15-477-3
US-09-866-379-10
US-09-866-379-10
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ALIGNMENTS

RESULT 1 US-09-259-214-2 ; Sequence 2, Application US/09259214A Patent NO. 6110719 ; GENERAL INFORMATION: APPLICANT: Kretz, Keith TITLE OF INVENTION: NOVEL PHYTASE FILE REFERENCE: DIVER1370-1 ; CURRENT APPLICATION NUMBER: US/09/259,214A ; CURRENT FILING DATE: 1999-03-01 ; EARLIER APPLICATION NUMBER: 08/910,798 ; EARLIER FILING DATE: 1997-08-13 ; NUMBER OF SEQ ID NOS: 4 ; SOFTMARE: FOSTORY OF SEQ ID NOS: 4 ; SEQ ID NO 2 ; LENGTH: 440 ; TYPE: PRT ; ORGANISM: Escherichia coli US-09-259-214-2

Query	Query Match Best Local Similarity	100.0%; Score 2302; DB 2; Length 440; arity 100.0%; Pred. No. 3.9e-234;	
Match	Matches 440; Conservative	.0,	0;
Ą	1 MKAII	MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60	0
용	1 MKAII	MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60	0
ş	61 TWPVI		120
용	61 TWPVI	TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 1	120
¥	121 AFAAC	AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180	90
F	121 AFAAC	AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 1	180
¥	181 RQTAE	-2	0
ğ	181 RQTAE	RQTAFRELERVINFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240	0
¥	241 EIFLI	EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300	8
岁	241 BIFLI	EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300	9
¥	301 LTPHE	LTBHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360	0
ğ	301 LTPHE	LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360	0
¥	361 RRLSI	RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420	0

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CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER FILING DATE: 1997-04-13
EARLIER FILING DATE: 1997-08-13
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EARLIER FILING DATE: 1999-03-01
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SOFTWARE: FastSEQ for Windows
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ORGANISM: Escherichia
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APPLICANT: KTECZ, Keith
TITIE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/02903
CURRENT APPLICATION NUMBER: US/09/291,931
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Escherichia
US-09-291-931-2
APPLICAMT: Kretz, Keith
FILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/02903
CURRENT APPLICATION NUMBER: US/09/580,51
CURRENT FILING DATE: 1999-05-25
FRIOR APPLICATION NUMBER: 09/318,528
FRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-26
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
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Best Local
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Pred. No. 3.9e-234;
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RESULT 5
US-09-866-379-2
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; ORGANISM: Escherichia
US-09-580-515-2
             FILE REFERENCE: DIVERLIATO-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-35
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
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Best Local Sim:
Matches 440;
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 440
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APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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Pred. No. 3.9e-234;
); Mismatches 0;
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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT APPLICATION NUMBER: US 09/860,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/290,214
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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; LENGTH: 440
; TYPE: PRT
; ORGANISM: Escherichia c
US-09-866-379-2
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US-09-866-379-8
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GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 440; Conservative (
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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Pred. No. 3.9e-234;
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RESULT 7
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; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-715-477-1
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                                                                                                                           Matches 429;
                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                 APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.5e-226;
0; Mismatches 3;
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Pred. No. 4.5e-227;
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; Sequence 1, Application US/10266041A
; Patent No. 6974690
; GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVED PHY
FILE REFERENCE: 19603/2798
; CURRENT APPLICATION NUMBER: US/10/266,041A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/127,032
; PRIOR FILING DATE: 1999-03-31
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 09/540,149
; PRIOR APPLICATION NUMBER: 09/540,149
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
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Best Local Similarity
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TYPE: PRT
ORGANISM: Escherichia
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                                                  EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
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                                                                                                                                    RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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Pred. No. 1.4e-225;
0; Mismatches 4;
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; LOCATION: (433)
; OTHER INFORMATION: Xaa at position 433 in this sequence is unknown
US-09-540-149A-1
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US-09-540-149A-1
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TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR PILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Escherichia
FEATURE:
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                        IVNEARIPACSL 432
                                                                  RRLSDNSQWIQVSLVFQTLQQWRDKTPLSLNTPPGEVKLTLAGCEERNAQGWCSLAGFTQ 420
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                                                                                                       LTPHPPQKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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IVNEARIPACSE 432
                                                   RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGPTQ
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Pred. No. 1.4e
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US-08-910-798-2
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                                                                        ; Sequence 2, Application U; Patent No. 5876997; GENERAL INFORMATION: APPLICANT: KRETZ; TITLE OF INVENTION: NUMBER OF SEQUENCES:
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RESULT 10

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

92037

CITY: La Jolla STATE: California COUNTRY: US

STREET:

4225 Executive Square,

Suite 1400

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C

NOVEL

US/08910798

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CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 199-11-18
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 432
TYPE: PRT
ROANISM: Escherichia coli
US-09-715-477-3
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APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE
FILE REFERENCE: 19603/4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 96.0%;
Best Local Similarity 98.6%;
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IVNEARIPACSL
                                                                       RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 2e-224;
2; Mismatches
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RESULT 12
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         GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GRAYTHERETY, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
                                                                                                                                                                         Sequence 10, Application US/09866379 Patent No. 6855365
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,798
FILING DATE: AUGUST 13,1997
CLASSIFICATION: 435
CLASSIFICATION: 435
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NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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REFERENCE: DIVER1370-7
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96.1%;
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Pred. No. 8.3e-223;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/866,379
CUBRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 430
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US-09-489-039A-7512
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Sequence 7512, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09/17,747
PRIOR APPLICATION NUMBER: US/09/17,747
PRIOR PILLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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Best Local
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Pred. No. 3.9e-217;
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; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13501
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13501
LENGTH: 522
TYPE: NEW
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LENGTH: 421
                                                                                                                                                                                                                                                                                                                        Query Match
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Best Local Similarity
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                    Local Similarity
120 EAFAAGLAFDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTG
                                                                          164 TEWTTHDGELTGHGYAAVVNKGRAEGOHYRQLGLL-QAGCPTAESIYVRASPLQRTRATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 WIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEA 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 LMKIEYVYÓSTEÓLKNADALTLQAÞÞQRVTLALNGCÞV-DDQGFCÞLETFKMVINEA 419
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                                                                                                                                                                                                                       2 KAILIPELSLLIPLTP-QSAFAQSEPELKLESVVIVSRHGVRAPTKAT-QLMQDVTPDAW 59
                                                                                                                                                                         GGLLRLFIACALPLLALQSAAA---ADWQLEKVVELGRHGIRPPTAGNREAIEAATGRPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAFAQSE----PE-LKLESVVIVSRHGVRAP-TKATQLMQDVTFDAWPTWPVKLGWLTPR
                                                                                                                          PTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTG 119
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                                                                                                                                                                                                                                                                     16.3%; Score 376; DB 2; Length 522; Llarity 25.8%; Pred. No. 1.8e-30; Conservative 75; Mismatches 209; Indels
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TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
PITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8:
SOFTWARE: PatentIn Ver.
SEQ ID NO 3
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 5.2%; Score 119; DB 2; Length 439; Local Similarity 21.7%; Pred. No. 0.002;
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                                                                                                                                                                                                                                                                                                                                                                                             59 -----WPTWPVKLGW--LTPRGGELIAYLG--HYQRQRLVADGLLAKKGCPQSGQVAII 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 PFLSLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPT----KATQLMQDVTPDA---
     HNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQ-----AYGVTLPTSVLFIA 323
                                                   KGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVP-----FIR 132
                                                                                                 QALPSEL--KVSADNVSLTGAVSLASMLTBIFLLQQAQGMPEPGWGRITDSHQWNTLLSL 271
                                                                                                                                                                                             COLDNANVIDAILSRAGGSI-ADFIGHRQTAFRELERVINFPQSNLCLKREKQDESCSLT 213
                                                                                                                                                                                                                                                                                              ADVDERTRKTGEAFAAGL------APDCAITVHTQADTSSPDPLFNPLKTGV 154
                                                                                                                                                  C----TKFEASQLGDEVAANFT-----ALFAP--DIRARAEKHLPGVTLT
                                                                                                                                                                                                                                                ASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVII-PESETFN----NTLDHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                PFFSLEDELSVSSKLPK---DCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG-QPDNTPPGGELV 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCPFQAAITALGQRIDRSSAPAVAM 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LERWRNAKSGERYLRVYFQAQGLDDLR-----RLQTPDAQHPMLRQEWHQPGCRQTDVGT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLT-----LAGCEERNAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRQA----LAPTIQLLKQAVC----QADKPCPIFDT-PWQVEQSKSGKTTISGLSVMANM
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TOMSCHY, Andrea
van LOON, Adolphus
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Result
No.
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abse/ABSSWEB spool/USI0601319/runat 12062006 180052 27516/app_query.fasta_1
-Q=/abse/ABSSWEB spool/USI0601319/runat 12062006 180052 27516/app_query.fasta_1
-DB=ESST QFMT=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORR=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=2000000000 -HOST=abse03p
-USER=USI0601319 @CGN 1 12067 @runat 12062006 180052 77516 -NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                       Score
     1044
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913
896
                                                                                       Query
Match
                                                                                                                                                                                                                                                EST: 2999: **
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2302
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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133	137.5	139.5	144.5	150	153	163	172	172.5	183	185.5	186	195	215	219.5	225	225	228.5	269	278	284	287	291	339	345.5	350.5	355	355	374.5	392		511.5	522	591.5	641	643	643	757	767	838	846	
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ALIGNMENTS

								COMMENT	JOURNAL	TITLE		AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BJ074127/c	RESULT 1
<pre>URL. http://xenopus.nibb.ac.jp.</pre>	The information of this clone is available through the following	Email: tshini@qenes.niq.ac.ip	Fax: 81-559-81-6855	Tel: 81-559-81-6856	1111 Yata, Mishima, Shizuoka 411-8540, Japan	National Institute of Genetics	Center For Genetic Resource Information	Contact: Tadasu Shin-i	Unpublished (2001)	Expressed genes in X. laevis embryo	Kohara, Y.	Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and	1 (bases 1 to 616)	Xenopodinae; Xenopus; Xenopus.	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Xenopus laevis	Xenopus laevis (African clawed frog)	EST.	BJ074127.1 GI:17504316	BJ074127	laevis cDNA clone XL090j06 5', mRNA sequence.	BJ074127 NIBB Mochii normalized Xenopus tailbud library Xenopus	BJ074127 616 bp mRNA linear EST 29-SEP-2003		

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RESULT 2
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Best Local Similarity:
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 ACCESSION
                                   DEFINITION
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PRI0142b_B11 - PR
pacificus var. Ca
survey sequence.
CL662734
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                                                                                                                                                                                                GlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsnThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                   ArgAlaGlyGlySerIleAlaAspPheThrGlyHisArgGlnThrAlaPheArgGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                             ProLeuLysThrGlyValCysGlnLeuAspAsnAlaAsnValThrAspAlaIleLeuSer
                                                                                                                                                  LeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrProGluValAlaArgSer
                                                                                                                                                                                                                                                                                        SerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspAsnValSer
                                                                                                                                                                                                                                                                                                                         GAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAA
                                                                                                                                                                                                                                                                                                                                     GluArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGlu
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                                                                                                               ArgAlaThrProLeu 293
                                                                                                                                                                                   CTGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAACACCTTG
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
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clone="XL090j06"
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                    953 bp DNA linear GSS 09-JUL-2004 PRI0142b.B21 (853) Mixed stage fosmid library of P. California Pristionchus pacificus genomic, genomic
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AUTHORS
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Class: fosmid ends.
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pristionchus pacificus
  GlnThrLeuGlnGlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGlu
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1036.00
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US-10-601-319-2 (1-440) x CL662734 (1-853)
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Pristionchus pacificus
Nucleic Acids Res. 32 (1),
14681447
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Email: rall:sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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Eukaryota; Metazoa, Nematoda, Chromadorea;
Neodiplogasteridae, Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTTGCTACAACGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTGGATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAGGATCACCGATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyArgIleThrAspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPhe
                                                                                                                                             GluLeuAsnTrpThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuVal
                                                                                                                                                                                                                             ThrSerValLeuPheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeu
                                                                                                                                                                                                                                                                                    ATCATGGCAGCGTTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCC
                                                                                                                                                                                                                                                                                                            IleMetAlaAlaLeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                TyrLeuLeuGlnArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeu
                                                         PheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPhe 376
                                                                                                                      GAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pristionchus p
/mol type="genomic DNA"
/strain="California"
/db xrefe="eaxon:54126"
/clone lib="Mixed stage f
var California"
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Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G. Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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SJAABUGG2 Adult SjC 7/94 Schietosoma japonicum cDNA similar to
pdb|1DKP|A Chain A, Crystal Structure Of Phytate Complex Of
Escherichia Coli Phytase At Ph 6.6. Phytate Is Bound With Its
3-Phosphate In The Active Site. Hg2+ Cation Acts As An
Intermolecular Bridge, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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EST.
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/tissue type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
/clone_lib="Adult sjc 7/94"
/clone_lib="Adult sjc 7/94"
/clone_lib="Adult sjc 7/94"
/note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed mex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oilgo dT
chromatography, using a kit from pharmcia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oilgo-dT-XhoI-primer and synthesized using
M-MLV reverse transcriptase. Second strand synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Schistosoma japonicum"
/mol_type="mRNA"
/strain="Chinese (Anhui) strain"
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clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, NO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

RESULT 4 CA093060 REFERENCE S 닭 Ś 문 ঠ 밁 5 밁 S 밁 Ś 밁 Ś 밁 S 밁 S KEYWORDS VERSION ACCESSION DEFINITION US-10-601-319-2 (1-440) x BU713770 (1-529) Query Match: Best Local Percent Similarity: Alignment Pred. No.: AUTHORS TITLE JOURNAL ORGANISM 421 364 361 344 301 324 241 304 181 284 121 264 244 LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 224 AlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe 243 481 61 Similarity: Saccharum officinarum Saccharum officinarum Saccharum officinarum Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Spermatophyta; Magnoliophyta; Liliopsida; Saccharum; Saccharum officinarum Vettore,A.L., da Silva,F.R., K The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-SCCCCL2001D10.b CL2 Saccharum CA093060.1 GI:34946367 CA093060 3', mRNA sequence. GATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTG AspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeu SerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArg GlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuPro GluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAlaLeuThrPro GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrPro AGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGT GGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTA GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu GGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCCC CATCCACCGCAAAAAACAGGCGTATGGTGTGACATTACCCCACTTCAGTGCTGTTTATCGCC HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla GAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT (bases 1 to 746) 1.08e-82 913.00 98.9% 98.9% 39.7% 746 bp mRNA-marum officinarum cDNA clone Length: Matches: Conservative: Mismatches: Indels: Kemper, B.L. 174 0 2 0 EST 23-SEP-2003 ne SCCCCL2001D10 528 399 323 480 420 360 343 300 240 303 283 120 263 60

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                                                                                                                                                                                                              439
                                                                                                                                                                                                                                284 GluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAlaLeuThrPro
                                                                                                                                                                                                                                                                                         379
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                                                                                                                                                                                                                                                                                                                                                                                                                                         259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 AlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 GluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSer
                       344
                                                                                             324
                                                                                                                                                                                                                                                                                                                            264
                                                                                                                                                                                                                                                                                                                                                                                                    244
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Fax: 55 19 3788 1089
Email: parruda@unicamp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br plate: 001 row: D column: 10 Seq primer: M13/Forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Arruda P
                                                                              GlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuPro
                                                                                                                                                            HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla
                                                                                                                                                                                                                                                                                                            GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrPro
                     GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu 363
                                                                                                                                                                                                                                                                                                                                                                                      LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis
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                                                                                                                                      CATCCACCGCANAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCC
                                                                                                                                                                                                              GAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC
                                                                                                                                                                                                                                                                                         CTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:4547"
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Mismatches:
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Best Local Similarity:
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clac; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CP326092 595 bp mRNA linear EST 18-AUG-
JMMT1--05-B09.g1 AtJMT-overexpressing transgenic rice lambda phay
cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
clone JMT1--05-B09, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF326092.1 GI:33800445
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                   SerLeuHigAsnAlaGlnPheTyrLeuLeuGlnArgThrProGluValAlaArgSerArg
GCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAG
                                                                      82 31 330 6193
82 31 321 6355
                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="maNA"
/culfivar="Nackdong"
/db xref="taxon:39947"
/db xref="taxon:39947"
/db xref="taxon:39947"
/clone="JMT1-05-B09"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone lib="AtJMT-overexpressing transgenic rice lambda phage CDNA library (JMT1)"
/clone lib="AtJMT-overexpressing transgenic rice lambda phage CDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZhP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2004)
Contact: D. Tagu
INRA Rennes
UMR B103P, BP 35327.
                                                                                                                                                                                                                                                          UMR Bi03P, BP 35327, F-35653 Le Rheu Cedex France Tel: +33.2.33.48.51.65
Fax: +33.2.33.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphi Genomics in collaboration with Genoscope FCR PRIMERS FORWARD: CAGGAAACAGCTATGACC Plate: 5 row: C column: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididea; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 895)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
CN762997
CN762997.1 GI:47536920
EST.
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Acyrthosiphon pisum
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IDOAAASDCO9RM1 ApMS
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/mol type="mRNA"

/cultivar="developmentstage"

/db xref="taxon:7029"

/clone="IDOAAA5DC09"
                                                                                                                                                                                                                                    row: C column: 9.
Location/Qualifiers
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the pea aphid Acyrthosiphon

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Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 868)
Hunter, M., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
Stern, D., Tagu, D. and Wincker, P.
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IDOAAA12DE01RM1 ApMS
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
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Unpublished (2004)
Contact: D. Tagu
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                                                                           GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IDOAAAIJDEO1"
/tlissue_type="whole insect"
/tlissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab host="XI.1-Blue"
/lab host="XI.1-Blue"
/clone_lb="ApMS"
/clone_lb="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
Sample name: IDOAAA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: (01/66/1999;
Soil conditions: Soil; Sowing date: (01/66/1999;
Harvesting date: (01/66/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction.; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"
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AUTHORS
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Baraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 864)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon
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Contact: D. Tagu
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Acyrthosiphon pisum
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                      ThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAlaLeu
  ACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTG-ATCAAGACAGCGTTG
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                                                                                                                                                                                                                                                                                                                  /note=Tvector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: IDDAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Acyrthosiphon pisum"

/mol type="mRNA"

/cultivar="developmentstage"

/db xref="taxon:7029"

/clone="IDOAAA1DF09"
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lab_host="XL1-Blue"
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RESULT 9
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AW036132
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                                                                                                                                                                                                                                                                                                                                                               Contact: CUGI
Clemson University Genomics
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Lycopersicon esculentum
Lycopersicon esculentum
Eycopersicon esculentum
Eycopersicon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eyermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
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/lab_host="XL1-Blue MRR'"
/clone_lib="tomato seed, TRAMU"
/clone_lib="tomato seed EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                     /db_xref="taxon:4081"
/clone="cLEE1E23"
/tissue_type="seeds"
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Lycopersicon esculentum
Lycopersicon esculentum
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B.,
Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C.,
Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato seed tissue
                                                                                                                                      100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
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383 bp mRNA linear EST 18-MAY-200 EST274510 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

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AW036134.1 GI:5894813
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                   /db_xref="taxon:4081"
/clone="clee1E23"
                                                   organism="Lycopersicon/mol_type="mRNA"
/cultivar="TA496"
/tissue_type="seeds"
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                         M11B12STM Arabidopsis developing seed Arabidopsis thaliana clone M11B12 5', mRNA sequence.
                                                  Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                          1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Narduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                               224 Biochemistry, Michigan State University,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerMetLeuThrGluIlePhe 243
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517
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/lab_host="XL1-Blue MRP'"
/clone_lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site
/note="Vector: pBlueScript SK(-); Directionally cXho1; CLEE - Tomato Seed EST Library. Directionally cCDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
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RESULT 12
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BU713769.1
EST.
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         Schistosoma japonicum
Schistosoma japonicum
Bukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea,
                                                                                                                       BU713769 531 bp mRNA linear EST 23-OCT-2003 SJARBUG01 Adult SjC 7/94 Schiattosoma japonicum cDNA similar to spl p07102 ppA ECOLI PERLIPLASMIC APPA PROTEIN PRECURSOR (INCLUDES: PHOSPHOANHYDRIDE PHOSPHOHYDROLASE (PH 2.5 ACID PHOSPHATASE) (AP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: benning@msu.edu
Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                        6-PHYTASE ], mRNA sequence.
                                                                                                                                                                                                                                                      ValSerLeuThrGlyAlaValSerLeuAlaSer 237
                                                                                                                                                                                                                                                                                                                   GluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGln
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                                                                                                                                                                                                                                      GTCTCATTAAGCGCTGCGGTAAGCCTCGCATCA
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/mol type="mRNA"
/ecoType="Columbia"
/db xref="taxon:3702"
/clone="M11B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Arabidopsis developing /note="Organ: Developing seed; Vect Site_1: EcoRI; Site_2: XhoII"
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/dev_stage="5-13 days
/lab_host="E.coli"
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                         244 LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 263
                                                                                                                                    224 AlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe
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Chinese National Human
351 Guo Shoujing Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J., Xu,X.N., Wang,S.Y., Pu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G. Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource Nat. Genet. 35 (2), 139-147 (2003)
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                                                                                                    GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /uev_bruge="Adult Worms"
//lab host="Mouse and rabbit"
//clone lib="Adult $jC 7/94"
//note="vector: Lambda ZaP-II XR.; Site 1: EcoR I; Site 2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from Pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-Xho1-primer and synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that small percentage, 2% to 3%, of the
clones contain inserts that appear to be highly homologous
to sequences from salmonoid fishes, as determined by
homology comparisons using BLAST and by Southern
hybridization analysis to genomic DNA from salmon (Sigma
Chemical Co., St. Louis, MO) under stringent washing
conditions. The remainder of the clones appear to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86-21-50801922
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/mol_type="mRNA"
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/dev_stage="Adult worms"
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25.7%
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Zhangjiang Hi-Tech Park, Pudong,
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Matches:
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133
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SOURCE
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VERSION
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CN759004/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       706 bp mRNA IDOAAA24BC04RM1 ApMS Acyrthosiphon pisum 5', mRNA sequence.
CN759004
                                                                                                                                                                                                                                                                                                                              UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.56
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2004)
Contact: D. Tagu
INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphididea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 706)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
                                                                                                                                                                                                                                                                        FORWARD: CAGGAAACAGCTATGACC
Plate: 24 row: C column: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgAspLysThrProLeuSerLeuAsnThrProProGlyGlu 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGCAGCCCGATAACACGCCCGCAGGAGCGGAACTGGATGTTTGAACGCTGGGCGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: IDOAAA; Plant growth place: Department of
                                                    /clone="ID0AAA24BC04"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XII1-Blue"
                     /clone_lib="ApMS"
/note="Vector: pB
                                                                                                                                                               /mol_type="mRNA"
/cultivar="developmentstage"
                                                                                                                                                                                                           organism="Acyrthosiphon pisum"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                              db_xref="taxon:7029"
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CDNA clone ID0AAA24BC04
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TITLE
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KEYWORDS
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AA545747/c
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 354)

Jia,L., Robey,P., Young,M., Schuler,G., Powell,J., Yang,L.,

Lennon,G., Hillier,L., Allen,M., Bowles,L., Geisel,S., Kucaba,T.,

Marra,M., Martin,J., Steptoe,M., Tan,F., Theising,B., Bowers,Y.,

Wylie,T., Waterston,R., Wilson,R. and Francomano,C.

WashU-MGB/NHGRI EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HBMSF1B4-REV Human Bone clone HBMSF1B4 5', mRNA
                                                                                                                                           National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda, Tel: 301-402-4877 Fax: 301-496-7157
                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Libin Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                 Medical Genetics Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA545747.1 GI:2307026
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                                                                                                    il: libin@helix.nih.gov
primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecology & Evolutionary Biology, Princeton University; soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                Location/Qualifiers
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Marrow Stromal Fibroblast
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Matches:
Conservative:
Mismatches:
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Homo sapiens cDNA
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RESULT 15
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Best Local Similarity:
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                                                                            Contact: Tadasu Shin-i
Center For Genetic Resource Information
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, v
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

[ (bases 1 to 707)
                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
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http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                 Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                             Expressed genes in X. laevis embryo Unpublished (2001)
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                                               The information
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/dev_stage="mixed"
/lab_host="XL1-Blue"
/clone_lib="Human Bone Marrow Stromal Fibroblast"
/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI"
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FEATURES

Search con Job time :	B 64	Qy Db	D Qy	QY Db	99 53	US-10-601-	Alignment Sc Pred. No.: Score: Score: Percent Simi Best Local S Query Match: DB:	BOUZG
Search completed: June 14, 2006, 15:26:30 Job time : 4992.33 secs	331 AsnLeuGlyGlyAla 335 	311 TyrGlyValThrLeuProThrSerValLeuPheIleAlaGlyHisAspThrAsnLeuAla 330 	291 ThrProLeuLeuAspLeuIleMetAlaAlaLeuThrProHisProProGlnLysGlnala 310 	271 LeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrProGluValAlaArgSerArgAla 290 	251 MetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsnThrLeuLeuSer 270 	US-10-601-319-2 (1-440) x BJ619443 (1-707)	Alignment Scores: 2.66e-34 Length: 707 Pred. No.: 442.00 Matches: 83 Percent Similarity: 97.6\$ Conservative: 0 Best Local Similarity: 97.6\$ Mismatches: 2 Query Match: 19.2\$ Indels: 0 Caps: 0	## Source 1707 Yorganism="Xenopus laevis" / Mol_type="mRNA" / Mol_type="mRNA" / Clone="txaxon:8355" / Clone="tx1189d24" / tissue_type="whole embryo" / dev stage="stage 10.5" / dev stage="stage 10.5" / Clone_lib="NIBB Mochii normalized Xenopus early gastrula library"

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Percent Similarity:
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2783
LENGTH: 3731
TYPE: DNA
ORGANISM: OTYZE SETIVE
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103280
DATABASE ENTRY DATE: 2002-08-28
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                                 ACA---TCCACCATGCATAATGCATTGAGGCCATTTTCATCGGAAGCACCTTCGCACCTA
                                                               ThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrPro-----
                                                                                                   CAGCCACAGAGCTATCCAGACACGAGTATGAGCTCATTATCACCATCC-----AAC
                                                                                                                                 GlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsn
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                                                                         TCAGGATATGTGCCGTGTTCA---CAGAATTCTGATCAAGTGATTAAT-----CGACCA 3054
CCIGCG
                                    ProAla 429
                                                                                                            AsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGlnIleValAsnGluAlaArgIle 427
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                                                          AlaileileAlaAspValAspGluArgThrArgLy8ThrGlyGluAlaPheAlaAlaGly
                                                                                   LeualaProAspCysAlaIleThrValHisThrGlnAlaAspThrSerSerProAspPro
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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Publication No. US20060123505A1
GENERAL INFORMATION:
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                                   -GlyGlyGluLeuValPheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGl 371
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE REFERENCE: MOA-A02051-US
FULE REFERENCE: MOA-A02051-US
CURRENT PLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR PLICATION NUMBER: UP 2002-203269
PRIOR PLICATION NUMBER: UP 2002-383870
PRIOR PLICATION NUMBER: UP 2002-183870
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Publication No. US20060123505A1
GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: AK100030
DATABASE ENTRY DATE: 2002-08-28
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ORGANISM: Oryza
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Sequence 34901, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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Publication No. US20060111297A1
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce
ITLE OF INVENTION: BLOOD FACTOR DOMAINS
FILE REFERENCE: 5270C
CURRENT APPLICATION NUMBER: US/11/297,134
CURRENT FILING DATE: 2005-12-08
PRIOR PILICATION NUMBER: PCT/US2005/018461
PRIOR APPLICATION NUMBER: DCT/US2005/018461
PRIOR PILING DATE: 2004-06-09
PRIOR PILING DATE: 2003-06-09
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Parentin version 3.3
SEQ ID NO 55
LENGTH: 1502
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Matches:
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Mismatches:
Indels:
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98.50
34.9%
22.1%
4.3%
                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                            LENGTH: 14756
                                                                                         ORGANISM: Hom
US-10-505-928-570
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SEQ ID NO 570
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335 TCTCCGACCTCACCAACCAGGTGACCGGTCTCAACGAGAAGCTCGTCAAATCCTTCAATC 594
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s95 GCATCGCCGACCTCGAGGACGACTCGGACGACGAGAGACCATTCGCACCATGTCGG 654
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/202-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12801
LENGTH: 3287
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK110149
DATABASE ENTRY DATE: 2001-12-06
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US-10-449-902-12801
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173 erIleAlaAspPheThrGlyHisArgGlnThrAlaPheArgGluLeuGluArgValLeuA 193
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CURRENT APPLICATION NUMBER: 405/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PATENTIN 3.2
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Publication No. US20060088532A1
GENERAL INFORMATION:
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	178 ThrGlyHisArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSer 197	187 TCGAACCATATCCAGACCTTCTTCAGGCTCGTCAAGACCGGCCAGTTC 234	AsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuPro 21	GACCTCATCGACTGGCGCAGCGTGTGTTTCGCTGCTGCCCCTCGCACATAGC		238 MetLeuThrGluIlePheLeufeuGlnGlnAlaGlnGlyMet 251	343 GCCACCGGGTCGCTGTTTGACCACATGCTTCAGCAGCTGCAGGAGCTGCAGCTGCTGATG 402	252 ProGluProGlyTrpGlyArglleThrAspSerHisGlnTrpAsn 266	403 GCGTCTGTGGGCCCGTCCACTTGCTCGGACGCCGAGGTCACCACGCTCAGGAACTACGTC 462	267 ThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrProGluValAla 286 ::::::	287 ArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAlaLeuThrProHis 304	523 GCTGCT	305 ProProGlnLysGlnAlaTyrGlyValThrLeuProThr	318HisAsp 326	595 AAGTGCTTCATCGAGATCTGGGACGCGCTGTTGGTGTCCAATGACCAGTTCCTCAACGAG 654	327 ThrasnLeualaaasnLeuGlyGlyalaLeuGluLeuAsnTrpThrLeuProGlyGlnPro 346	347 Asp	358 GluArgTrpArgArgLeuserAspAsnSerGlnTrpIle 370	GINVAISerLeuvalPheGInThrLeuGInGlnMetArgAspLysThrProLeu 38 GINVAISerLeuvalPheGInThrLeuGInGlnMetArgAspLysThrProLeu 38 [CICCICCGAGICCCACCACCACAAICIGCIGCAGGACAACAICIC 93	Alaginglymercysserieualagiyphethrdin ::: GCacGactigactorgaccticcagga	429 AlaCysSerLeuArgSerHigHisHisHis 439 	NT 8 0-449-902-12801 squence 12801, Application US/10449902 blication No. US20066123505A1	GENERAL INFORMATION: ; APPLICANT: National Institute of Agrobiological Sciences.
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Qy 273 snalaGlnPheTyrĻeuLeuGlnA 281	Db 713 CATCCACAAAAAGAGGCTGATCCCTGCTCTCCACCGCCACAGGCCCGACACTGCACTCCC 654	Qy 281 rgThrProGluValAlaArgSerArgAlaThrProLeuLeuAgpLeuIleMetAlaAlaL 301	653 AGACCCTGGGGGCCCTTGCCCGGCACCGCCCTTGCAGCCTAGGGCTCCAGGCGAAAG	Dy sol euinferchieferoficherotingschaltstratyfolyvalinkleuprofinkservalleup 321 The sol reducing response solutions and solutions solut	321 hellealaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpT		Qy 341 hrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpA 361	Db 526	Qy 361 rgArg-LeuSerAspAsnSerGlnTrplleGlnValSerLeuValPhe 376	Db 492 CCAGGTCTGTGCCACATGTCATGTGAGGAACCCTCGAGTTC 445 RESULT 7	US-11-217-529-274 ; Sequence 274, Application US/11217529 ; Publication No. 1522060099612A1	; GENERAL INFORMATION:	,	; APPLICANT: FUJIMIRA, TOMOKO ; APPLICANT: ASHIKARI, TOSHIHIKO : TITIE OF INVENTION: METHODS FOR ANALYZING GENES OF INDIREPIAL. VERSETS	FILE CONTROL STATES AND STATES OF THE STATES	CURRENT FILING DATE: 2005-09-02; PRIOR FILING DATE: 2006-09-02; PRIOR FILING DATE: 2004-09-02;	; NOWHER OF SEQ 1D NOS: 197023 ; SOFTWARE: PatentIn version 3.3 ; SEQ ID NO 274 ; LENGTH: 2259	; life: DNA ; ORGANISM: Saccharomyces pastorianus US-11-217-529-274	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: 23.3\$ Conservative: 45 Best Local Similarity: 23.8\$ Mismatches: 138 Query Match: 7.4\$ Gaps: 21	US-10-601-319-2 (1-440) x US-11-217-529-274 (1-2259)	Qy 101 GlnSerGlyGlnValAlallelleAlaAspValAspGluArgThrArgLysThrGlyGlu 120 Db 7 CAGAGCAACAAGATCGCGTACGTGCTGAACTCCGACACGCAGGAGGCCGGCGAG 60	Qy 121 AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGln 137 ::	Qy 138 AlaAspThrSerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeu 157 Db 118GTCAAGGAALTS 129	AspAsnAlaAsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPhe

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4495 TICACCCAIGTGGCCCCCAAGCTGGCTTGTACCACTGCCAGGCTGAGCTCCCCGCC 4554
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|CTGAGCCAGGGTGGATGTGCCTGAAGCACAGCGCTGAACCTGAGCTGTCGCCTCCCT
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                                                        Glu---ArgValLeuAsnPheProGlnSerAsn----
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Publication No. US20060105376A1
GENERAL INPORMATRON:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTYON: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
FRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1957
LENGTH: 1945
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Best Local Similarity:
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US-11-293-697-1957
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                GAGACTGGCATCCGGCCTGGAGAGATGATAGGGGGGCTCCAAGGCCCAAGGTGGCCACCCC 418
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ProGluLeuLysLeuGluSerValValIleValSerArgHisGlyValArgAlaProThr
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## Sequence 5, Application US/11270040

## Sequence 5, Application US/11270040

## Sequence 5, Application No. US2006011076241

## Sequence 7, Application No. US2006011076241

## Sequence 7, Application No. US2006011076241

## APPLICANT: Kapil, Sanjay

## APPLICANT: Kapil, Sanjay

## APPLICANT: Kapil, Sanjay

## APPLICANT: Kapil, Sanjay

## TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY

## TITLE OF INVENTION: SYNDROME VIRUS RECEPTOR COMPONENTS AND USES THEREOF

## TITLE OF INVENTION: SYNDROME US/11/270,040

## CURRENT APPLICATION NUMBER: 05/680,297

## PRIOR PILLING DATE: 2005-05-12

## PRIOR PILLING DATE: 2005-05-12

## PRIOR PILLING DATE: 2004-11-10

## NUMBER OF SEQ ID NOS: 8

## SOOFTWARE: FastSEQ for Windows Version 4.0

## TEACH OF THE OF
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329 uAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuProGlyGlnProAspAsnTh 349
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1991 GTTGCCCTTCTTGCCGAGGCTGACGGTGTACTCGAGGCGGAGCTGCTTGAGCTCCTC 1932
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Matches:
Conservative:
Mismatches:
Indels:
                                                                   --CysProGlnSerGlyGln---
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Sequence 189, Application US/11145307A

Publication No. US20060094035A1

GENERAL INFORMATION:
APPLICANT: Arcturus Bioscience, Inc.
APPLICANT: Rilander, Mark G.
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Identification of Tumors
FILE REFERENCE: 022041-002020US
CURRENT PRILING DATE: 2005-06-03

PRIOR APPLICATION NUMBER: US 60/577,084
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SOFTWARE: Patentin version 3.1
SEQ ID NO 189
LENGTH: 2711
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ORGANISM: Homo sapiens
US-11-145-307A-189
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CONA AND USES THEREOF
FILE REPERBRÜCE: MOA-AQ205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR PLING DATE: 2002-15-20
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 7723
LENGTH: 2822
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                           uleuGluArgValLeuAsnPheProGlnSerAsnLeu---CysLeuLysArgGluLysGl
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Publication No. US20060123505A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK105071
JDATABASE ENTRY DATE: 2002-08-28
US-10-449-902-7723
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Best Local Similarity:
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US-10-449-902-7723/c
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US-10-449-902-21879/c
; Sequence 21879, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.
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TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT PILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
FRIOR APPLICATION NUMBER: JP 2002-203269
FRIOR FILING DATE: 2002-05-30
FRIOR FILING DATE: 2002-05-30
FRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: PATENTIAN Ver. 2.1
SEQ ID NO 21879
LENGTH: 1470
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Best Local Similarity:
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DB:
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK07:
DATABASE ENTRY DATE: 2001-12-06
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                                                                                      GATGTCCTCCGTCTGGATCTCCTGGTTCATGTTGTAGAGCACCTCCACCAGCGCCTCCGA
                                                                                                                           ---ValCysGlnLeuAsp---AsnAlaAsnValThrAspAlaIleLeuSerArg-----
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                                                                                                                                                                                                         --ProLeuPheAsnProLeuLysThrGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
          ------CACCGCCTCCTGCGCCCGCCCCCAC
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-GluAlaPhe

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Minimum DB
Maximum DB
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10601319/runat_12062006_180105_27789/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10601319/runat_12062006_180105_27789/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -HOST=abss03h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
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         a
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                                                                                                                       000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -USER=US10601319 @CGN 1 1 28 @runat 12062006 180105 27789 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                      is the number of results predicted by chance to have a ater than or equal to the score of the result being printed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xgapop 10.0 , 1
Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                           Published_Applications NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US01_NEW_PUB.seq:*
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       Maximum Match
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     1482
1470
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Ygapext
Fgapext
Delext
                                                                777666
 US-10-449-902-14217

US-10-449-902-21879

US-10-449-902-7723

US-11-145-307A-189

US-11-270-040-5

US-11-270-040-5

US-11-270-507-1957

US-11-271-529-274

US-10-505-928-570
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4595.351 Million cell updates/sec
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Biocceleration Ltd.
                                                                                                                                                                                                                                                                                       score distribution.
Sequence 21879, A
Sequence 7723, App
Sequence 189, App
Sequence 5, Appli
Sequence 1957, Ap
Sequence 274, App
Sequence 12801, Ap
Sequence 570, App
                                                                                                                                                                                             Description
                                                                                                                                  Sequence 14217, A
Sequence 21879, A
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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D	σ	7	7	σ	7	σ	7	σ	7	7	0	σ	0	9	7	7	6	σ	0	7	σ	0	1	7	σ	σ	7	σ	7	σ	σ	σ	σ	თ	7
-10-449-902-115	US-10-449-902-22201	-11-293-697-81	-11-293-697-51	-10-449-902-114	-11-217-529-27	-10-489-730-1	-11-118-524-	-10-449-902-12	US-11-293-697-315	-11-293-697-12	-10-449-902-2666	-10-449-902-13	-10-449-902-2201	-10-449-902-14	-11-293-697-14	-11-293-697-94	-10-449-902-16	-10-953-349-82	-10-511-937-3	-11-293-697-10	-10-449-902-201	-10-528-659-	-09-949-9	-11-284-978-1	-10-501-834-	-10-511-937-	-11-293-697-	-449-902-	S-11-293-697-148	-10-449-902-2783	-10-449-902-2458	-10-449-902-2692	-10-449-90	-10-953-349-3490	97-134-
equence 11507,	quence 22201	equence 815, Ap	equence 518, Ap	equence 11403,	ence 2750, A	INFORMAT	Sequence 1, Appli	1265	315, Ap	1200	2666	13489,	22017,	1494,	1467, F	946, Ar	1613	8294, A	358,	1085	2012	6	Sequence 71, Appl	equence 14, App	equence 1,	e 543, Ap	equence 841, Ap	equence 1265	e 1489, A	equence 27838,	equence 2458	equence 26929,	equence 20112,	equence 34901,	Sequence 55, Appl

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ALIGNMENTS

RESULT 1

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US-10-449-902-14217/c

| Sequence 14217, Application US/10449902
| Publication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: Bio-oriented Technology Research Advancement Institution.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: Foundation for Advancement of International Science.
| TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
| FILE REFERENCE: MOA-A0205Y1-US
| CURRENT FILING DATE: 2002-05-30
| PRIOR APPLICATION NUMBER: US/10/449,902
| CURRENT FILING DATE: 2002-05-30
| PRIOR APPLICATION NUMBER: UP 2002-203269
| PRIOR APPLICATION NUMBER: UP 2002-383870
| PRIOR APPLICATION NUMBER: 2002-12-11
| SEQ ID NO 14217
| SEQ ID NO 14217
| LENGTH: 1482
| TYPE: DNA Oryza sativa |
| PUBLICATION INFORMATION: |
| DATABASE ACCESSION NUMBER: AK064835 |
| DATABASE ACCES
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Appli Appli Appli Appli

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number

Searched:

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Sequence 7, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
     Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 7, Appli
Sequence 5, Appli
Sequence 9338, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25689, A Sequence 11, Appl Sequence 41608, A Sequence 3, Appli Sequence 1, Appli Sequence 9, Appli
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Sequence 3181, Ap
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Sequence 30120,
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Patent No. US20010055788A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: REPERIOR:

APPLICANT: NUMBER: US/09/777,566A

CURRENT APPLICATION NUMBER: US/09/777,566A

CURRENT APPLICATION NUMBER: US/09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR PELING DATE: 1999-03-01

PRIOR PELING DATE: 1999-03-01

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 1

LENGTH: 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 US-10-334-672-4

7 US-10-334-671-4

10 US-10-450-763-25699

6 US-10-021-723A-11

8 US-10-021-723A-3

6 US-10-021-723A-3

6 US-10-021-723A-3

6 US-10-021-723A-3

10 US-10-450-763-386

10 US-10-450-763-34447

10 US-10-450-763-30120
3 US-09-866-379-1
6 US-10-034-985-1
8 US-10-601-319-1
10 US-10-933-115-1
3 US-09-866-379-7
6 US-10-156-660-3
8 US-10-156-660-3
10 US-10-933-115-7
10 US-10-933-115-7
14 US-11-056-379-9
6 US-10-061-319-6
7 US-10-286-041-9
7 US-10-286-041-9
1 US-10-286-041-9
1 US-10-286-041-9
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1 US-10-286-041-9
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1 US-10-284-962-1
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1 US-10-10-10-93-115-6
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US-10-021-723A-5
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1196.5
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760
759.5
708
657
657
657
472.5
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USOO_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USOO_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USOO_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USOO_PUBCOMB.seq:*
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-MODEL=Frame+ par.model -DEV=xlp
-Q=\langle bass/ABSS\frame = par.model -DEV=xlp
-Q=\langle bass/ABSS\frame = par.model -DEV=xlp
-Q=\langle bass/ABSS\frame = par.model -DEV=xlp
-DB=Published Applications NA Main -QFNT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
-LOOPCI=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.014 -LIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss06p
-NSR=USIG0601319 @CGN 1 1 3524 @runat 12062006 180103 27735 -NCFU=6 -ICFU=3
-NO MMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                        (without alignments) 5637.400 Million cell updates/sec
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                                                                                                                                                                                                         US-10-601-319-2
2302
1 MKAILIPPLSLLIPLTPQSA......IVNEARIPACSLRSHHHHHH 440
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                                                                                                                                 June 14, 2006, 14:19:34 ; Search time 1438.58 Seconds
                       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                              - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                    18892170 seqs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length DB
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1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCACCATCACCATCAC 1320
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                                                                                                                                                 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320
       GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840
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NAME/KEY: misc_feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n is any nucleotide
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LOCATION: (1)..(1323)
OTHER INFORMATION:
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) ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1320)

; LOCATION: (1)..(1320)

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; OTHER INFORMATION: n is any nucleotide

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TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
FURENT APPLICATION NUMBER: US/10/034,985
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR PILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 1
LENGTHRE: FRAESEQ for Windows Version 4.0
SEQ ID NO 1
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ORGANISM: Bscherichia coli
FEATURE:
NAME/KEY: CDS

LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)

OTHER INFORMATION: n = A,T,C ox
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CAGTCTGGTCAGGTCGCGGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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                              GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
                                                                                                              SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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Sequence 1, Application US/10601319
Publication No. US20040091968A1
GENERAL INPORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevith A.
APPLICANT: Gray, Kevith A.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
ITILE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKI
TITLE OF INVENTION: AND USING THEM
FILE REPRENCE: 09010-02011
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILING DATE: 2000-05-25
PRIOR PLILING DATE: 1099-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR PLILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR PLILING DATE: 1999-04-13
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Matches:
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NAME/KEY: CDS
LOCATION: (1)...(1320)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 216
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Gray, Ketth A.
APPLICANT: Gray, Ketth A.
APPLICANT: Barret, James B.
APPLICANT: Barret, James B.
APPLICANT: Graver, James B.
APPLICANT: Govern A.
APPLICANT: Govern A.
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES TITLE OF INVENTION: THERBOX
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR APPLICATION NUMBER: US/09/806,515
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-03-04-13
PRIOR PILING DATE: 1999-03-04-13
PRIOR PILING DATE: 1999-03-04-13
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 216
OTHER INFORMATION: n = A,T,C or G
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US-10-601-319-2 (1-440) x US-10-933-115-1 (1-1323)
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Sequence 1, Application US/10933115
Publication No. US20050281792A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.

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Percent Similarity:
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Query Match:
DB:
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Pred. No.:
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                                          TCCAGTCCCGATCCGTTATTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGC
                                                                                                        ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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Sequence 7167, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari

10-282-122A-7167

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APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Will History
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA. 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-36
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/255,625
PRIOR PILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-11
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LOCATION: (1). (1901)
OTHER INFORMATION: n is any
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Best Local Similarity:
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ThrLeuproGlyGlnProAspAsnThrProProGlyGlyGlyLeuValPheGluArgTrp 360
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                                                                      AsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180
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                                   AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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Sequence 7, Application US/09866379; Patent No. US20020136754A1; GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith

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APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRET, James
APPLICANT: GARRET, James
APPLICANT: O'DONGGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US 09/66,379
CURRENT FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-25
PRIOR PELICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR PELICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-04-13
PRIOR PLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 7
LENGTH: 1901
TWDE: NAA
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181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200
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LOCATION: 403
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                          TYPE: DNA ORGANISM: Escherichia coli
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NAME/KEY: CDS
LOCATION: (188) ... (1483)
FEATURE:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                               LENGTH: 1901
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US-10-156-660-3
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                                                                             CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                           LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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                                 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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; Publication No. US20030103958A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Barton, Nelson R.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Garret, James B.
; APPLICANT: Garret, James B.
; APPLICANT: HIVENTON: ENTRASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: PHYTASES, US OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REPERENCE: 09010-029007
; CURRENT APPLICATION NUMBER: US/10/156,660
; CURRENT FILING DAIR: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/866,379
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161 AsnValThrAspAlalleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180
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PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
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ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 403
OTHER INFORMATION: n = A,T,C or
US-10-601-319-7
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81 GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100
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PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION WUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR PLING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 10
SEQ ID NO 7
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PRIOR FILING DATE: 1999-0J-04,
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 1901
FEATURE: NAA
ORGANISM: Escherichia coli
FRATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 403
OTHER INFORMATION: n = A,T,C or G
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                                                                                          LysvalSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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                                                          JUNEAU TO SEQUENCE TO APPLICATION US/10933115

PUBLICATION NO US20050281792A1

FORDERAL THRORMATION:

APPLICANT: Short, Jaw M.

APPLICANT: Short, Jaw M.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: O Donoghue, Bileen

APPLICANT: Mathur, Exic J.

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES

TITLE OF INVENTION: THERROF

TITLE OF SOURCES: 56462001822

CURRENT APPLICATION NUMBER: US/09/866,379

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/291,931

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ORGANISM: Escherichia coli app
FRATURE:
NAME/KEY: misc feature
LOCATION: (403)...(403)
OTHER INFORMATION: n is any nu
US-11-056-354-3
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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                                                                                  GAGATATTTCTCCTGCAACAAGCACAGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 967
                                                                                                                                    261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280
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                        PhelleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
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APPLICANT: Short, Jay M.
APPLICANT: Ketz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, James B.
APPLICANT: O'Donoghue, Elleen
APPLICANT: O'Donoghue, Elleen
APPLICANT: O'Donoghue, Elleen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEM
TILLE APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
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TYPE: DNA
ORGANISM: Escherichia coli
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Best Local Similarity: 99.3% Mismatches: 3 Query Match: 96.7% Indels: 0 DB: 3 Gaps:	-10-601-319-2 (1-440) x US-09-866-379-9 (1-1901)	Qy 1 MetlysAlaileLeuileProPheLeuSerLeuIeProJeuThrProGinSerAla 20 	Qy 21 PheAlaGlnSerGluDroGluLeuLy8LeuGluSerValVal11eValSerArgHisGly 40	Qy 41 ValargalaprothriysalathrGinieuMetGinaspValthrProAspAlatrpPro 60	Oy 61 ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGlyGluLeuIleAlaTyrLeu 80	Qy 81 GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100	Qy 101 GlnSerGlyGlnValAlallelleAlaAspValAspGluArgThrArgLysThrGlyGlu 120	Oy 121 AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140	Qy 141 SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160	Qy 161 AsnValThrAspAla11eLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180	Oy 181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200	201 LeulysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 2 	Qy 221 LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	Qy 241 GluilePheLeuLeuGinGlnAlaGlnGlyMet FroGluProGlyTrpGlyArgileThr 260	Qy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuWisAsnAlaGlnPheTyrLeuLeuGln 280	Qy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 3	Db 1088 TTGACGCCCATCCACGCAAAACAGGCGTATGGTGACATTACCCACTTCAGTGTG 1147 Qy 321 PheIlealaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	
	Qy 301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320	Qy 321 PhellealaGlyHisAspThrAsnLeualaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340 L148 TTTATCGCCGAACACAAATCTGGAAATCTGGGCGCACTGGACTCAACTG 1207	341 ThrieuproGlyGlnProAspAsnThrProProGlyGlyGluGeuValPheGluArgTrp	361 ArgArgLeuSerAspAsnSerGlnTrplleGlnValSerLeuValPheGlnThrLeuGln 38	381 GluMetArgAspLysThrProLeuSerleuAsmThrProProGlyGluValLysLeuThr 4 1328 CaGarGGGTGARAAATH	401 LeuAlaGlyCysGludluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 42 [1388 421 421	SULT 14 -09-866-379-9	E SE	; APPLICANT: SHORT, Jay ; APPLICANT: KRETZ, Keith ; APPLICANT: GRAY, Kevin ; APPLICANT: BARTON, Nelson	; AFFLICANT: GARKELT, James ; APPLICANT: O'DONOGHUE, Bileen ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF ; FILE REFERENCE: DIVER1370-7	NT APPLICATION NUMBER: US/09/866, NT FILING DATE: 2001-05-24 APPLICATION NUMBER: US 09/580,51 FILING DATE: 2000-05-25	; PRIOR APPLICATION NUMBER: US 09/318,528 ; PRIOR FILING DATE: 1999-06-25 ; PRIOR PAPLICATION NUMBER: US 09/291,931 ; PRIOR FILING DATE: 1999-04-13	; PRIOR APPLICATION NUMBER: US 09/259,214 ; PRIOR FILING DATE: 1999-03-01 ; PRIOR APPLICATION NUMBER: US 08/910,798 ; PRIOR FILING DATE: 1997-08-13	 NUMBER OF SEQ ID NOS: 10 SCPTWARE: PatentIn version 3.1 SEQ ID NO 9 LENGTH: 1901 	; TYPE: DNA ; ORGANISM: Bscherichia coli ; FEATURE: . NAME/FEV. misc feature	; COCATION: (1)(1901) ; OTHER INFORMATION: n is any nucleotide US-09-866-379-9	Alignment Scores: 2.27e-252 Length: 1901 Pred. No.: 2226.00 Matches: 429 Score: 99.3* Conservative: 0	

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Job time : 1468.58 secs
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                                                  ArgargLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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           ThrieuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp
                                                                                                                                                                                                                                       Sequence 9, Application US/10266041;
Sequence 9, Application US/10266041;
Publication No. US20030072844A1
GENERAL INFORMATION:
APPLICANT: Lel, Xingen
TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/10/266,041
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/09/540,149
PRIOR PILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 9
LENGTH: 1489
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US-09-944-119-1

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US-09-765-111A-24
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Patent No. 6110719
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVERI370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
BARLIER APPLICATION UNDRER: 08/910,798
BARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
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| NAMB/KEY: CDS
| LOCATION: (1)...(1320)
| NAME/KEY: misc_feature
| LOCATION: (1)...(1323)
| OTHER INFORMATION: n = A,T,C or G
US-09-259-214-1
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Fatent No. 6183740
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PHYTASE
FILE REPERENCE: 0910/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT PILING DATE: 1999-05-25
EARLIER PILING DATE: 1999-04-13
EARLIER PILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER PILING DATE: 1999-03-01
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ORGANISM: Escherichia coli
PRATURE:
NAME/KEY: CDS
LOCATION: (1) ... (1320)
NAME/KEY: misc_feature
LOCATION: (1) ... (1323)
OTHER INFORMATION: n = A,T,C or G
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Patent No. 6190897
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT PILING DATE: 1999-04-13
EARLIER PILING DATE: 1999-04-13
EARLIER FILING DATE: 1999-04-13
EARLIER FILING DATE: 1999-03-01
MUMBER OF SEQ ID NOS: 4
SOFTWARE: FREESE 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PABLEGE FOR WINGOWS Version 4.0
SENGTH: 1323 Ö or 1.05e-233 2302.00 100.0% 100.0% 100.0% A, T, C | FEATURE: | NAME/KEY: CDS | LOCATION: (1)...(1320) | NAME/KEY: misc_feature | LOCATION: (1)...(1323) | OTHER INFORMATION: n = A US-09-291-931-1 TYPE: DNA ORGANISM: Escherichia Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 급 121 81 241 101 301 121 361 141 161 421

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 SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                     ORGANISM: Escherichia coli
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NAME/KEY: CDS
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OTHER INFORMATION: n = A,T,C ox
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AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540
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                                     ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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OTHER INFORMATION: n is
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Query Match:
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Fatent No. 685365
Fatent No. 685365
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: MUMBER: US/09/866,379
CURRENT APPLICATION NUMBER: US 09/580,515
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-04-13
FRIOR PELING DATE: 1999-04-13
FRIOR PELING DATE: 1999-04-13
FRIOR PELING DATE: 1999-03-01
FRIOR APPLICATION NUMBER: US 09/259,214
FRIOR PELING DATE: 1999-03-01
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ORGANISM: Bscherichia coli
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LOCATION: (1)...(1323)
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Matches:
Conservative:
Mismatches:
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                                                              ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGGTGAAGCTAATCGCCTATCTC
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                                                ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
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Sequence 9, Application US/09866379

Patent No. 6855365

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORY, Jay

APPLICANT: SHORY, Jay

APPLICANT: BARTON, Nelson

APPLICANT: GRAY, Kevin

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

FILE REFERENCE: DIVERIATOO-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2001-05-24

FRIOR FILING DATE: 1999-04-13

FRIOR PILING DATE: 1999-04-13
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Matches:
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                                                      .082 TTGACGCCCCATCCACCGCAAAAAACAGGCGTATGGTGTGAGACATTACCCACTTCAGTGCTGTG
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   AsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                  AACGTGACTGACTGACGCGATCCTCAGCAGGGCAGGGACGTCAATTGCTGACTTTACCGGGCAT
                                                                                                               LeuLyBArgGluLyBGlnAspGluSerCyBSerLeuThrGlnAlaLeuProSerGluLeu
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LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
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Pacent No. 6511699
GENERAL INFORMATION:
APPLICANT: Lel, Xingen
TITLE OF INVENTION: EXZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR PILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
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Conservative:
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ORGANISM: Escherichia coli
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Best Local Similarity:
Query Match:
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                              LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320
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Sequence 6, Application US/09866379

Patent No. 6855365

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORY: Jay
APPLICANT: KRETZ, Kevin
APPLICANT: RARY, Kevin
APPLICANT: GARRETY, James
APPLICANT: OF ONOGHUS, Elleen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FRICARENT APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR PLING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
SOFTWARKE: PALENTIN NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
SOFTWARKE: PALENTIN VORSER: US 08/910,798
NUMBER OF SEQ ID NOS: 10
SOFTWARKE: PALENTIN VORSER: US 08/910,798
TYPR: NUM
                                             GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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OTHER INFORMATION: n is any nucleotide
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LOCATION: (1)..(1901)
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Percent Similarity:
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Mismatches:
Indels:
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LENGTH: 1489
TYPE: DNA
ORGANISM: Escherichia coli
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Patent No. 6441370

GENERAL INFORMATION:

APPLICANT: Lei, Xingen

TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE

FILE REFERENCE: 19603/4031

CURRENT APPLICATION NUMBER: US/09/715,477

CURRENT PALIAN DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/166,179

PRIOR FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2.
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TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESC
FILE REFERENCE: 19603/4031
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: 06/166,179
PRIOR PILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                        IleValAsnGluAlaArgIleProAlaCysSerLeu 432
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US-09-715-477-4
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ADDRESSER: ALSH & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: 4216crnia
COUNTRY: US
ZIP: 92037
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
ATCORNEY/AGENT INFORMATION:
NAVE: HALLE, PH.D., LIGA A.
REGISTRATION: WUMBER: 38,347
REJECOMMUNICATION NUMBER: 38,347
REJECOMMUNICATION NUMBER: 38,347
REJECTATION  1272 DASS DID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 DASS PAIRS
TUNDER: NUCLEIC acid
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TITLE OF INVENTION: NOVEL PHYTASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08910798
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IMMEDIATE SOURCE:
CLONE: PHYTASE
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                                427 CCGGTGCATCACCAGCCTCAGATGGGCACCATGGACCCGACCTTCAACCCGGTTATTACC 486
                                                                                                                                    GlyvalCysGlnLeuAspAsnAlaAsnValThrAspAlaIle---LeuSerArgAlaGly 171
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547 ATGCAGTTGACCGAG--------AGCTACAAGCTGCTGCAGACGATG 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaThrProLeuLeuAspLeuIleMetAlaAlaLeuThrProHisProProGlnLysGln 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 AlaTyrGlyValThrLeuProThrSerValLeuPheIleAlaGlyHisAspThrAsnLeu 329
                GluargThrArgLysThrGlyGluAlaPheAlaAlaGlyLeuAlaProAspCysAlaIle 132
                                                                                                                                                                                                 GlySerlleAlaAspPheThrGlyHisArgGlnThrAlaPheArgGluLeuGluArgVal 191
                                                                                                                                                                                                                                                                                                                           LeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspAsnValSerLeuThrGly 231
                                                                                                                                                                                                                                                                                                                                                                                        232 AlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeuGlnGlnAlaGlnGlyMet 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 AAGCTGAAAATGGCTATCAGGATAGTCTGTTTACCTCGGTGGCGGTGGCGCAAAACGTC 873
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creaggeagagaraagatacctttagggccggttatcagcaggaggccgggagggccgga
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Job time : 252.541 secs
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Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709.200401
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 341
                                                                                                                                                                                                                                                                                                            CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1149
                                                                                                                       ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380
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| CTGGTGACCAGCGGCGAGTGCCCGGGAAAACGCGGTTTATGCCTACGCTAACAGCCTG 366
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ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp
                                                                               ACGCTTCCCGGTCAGCCGGGTAACACGCCGCCAGGTGGAACTGGTGTTTGAACGCTGG
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ORGANISM: Klebsiella pneumoniae
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48.7%
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Best Local Similarity:
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US-09-489-039A-341
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Add19445 E. coli B
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Ad650303 Escherich
Ad650301 Kangaroo
Ad450301 Kangaroo
Ad4116137 Escherich
Ad41949 E. coli B
Ad281949 E. coli B
Ad281949 E. coli B
Ad2819 Escherich
Ad68019 Escherich
Ad650297 Escherich
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nutrition; ds.
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                    GluilePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArglleThr
                                                                                                                                                                                            ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla
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                                                              Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from
                                                                                                                                                                                       The present sequence encodes a phytase enzyme from Escherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate in phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients
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                                                                    GAGATATTTCTCCTGCAACAAGAAGACAGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                            CTTAAACGTGAGAAACACGAAGGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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                                                                                                                            release biocompatible composition which comprises an agent (enzymes such as phytase, amylase, esterase, protease) that assists in digestion. The biocompatible composition is effective upon oral consumption and release in the digestive tract of a subject. The distary aids are useful for delivering enzymes, therapeutics, medicine and agents to an organism. The use of enzymes and other agents in digestive aids of livestock or domesticated animals not only improves the animal's health and life expectancy but also assists in increasing the health of livestock or the production of foodstuffs from livestock. The present sequence is Escherichia coll phytase DNA
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                                    New dietary aids comprising sustained release biocompatible compositions, comprise agent that assists in digestion, useful for delivering enzymes, therapeutics, medicine or agents to an organism.
                                                                                                               present invention relates to novel dietary aids comprising sustained
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The patent discloses recombinant bacterial phytase from Bscherichia colicated apply phytase. The enzyme has phytase activity and improved procease tolerance when compared with wild-type phytase. It has improved procease tability at low pH. The recombinant phytase is useful for improving the activity at low pH. The recombinant phytase is useful for improving the around value of phytate-containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are also used for generating recombinant digestive system life forms, for producing or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of environmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral supplements, enzymes or therapeutic drugs for animals from the deal the increasing the amount calories and nutrients present in the feed.
                                                                                                                                                                                                                       New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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                 24-MAY-2001; 2001WO-US017118
                                                    25-MAY-2000; 2000US-00580515
                                                                                                                             Short JM, Kretz KA,
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Best Local Similarity:
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                                       SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
                                                          TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                                                                             AsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                                                                                                                                                                 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
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Phytase; ds; gene; phytate; appA gene; animal feed; inorganic phosphate; digestion enhancement; transgenic; thermal tolerance; protease stability
                                                                                                                                                                         Garrett JB;
                                                                                                                                                                        Gray KA, Barton NR,
                            ocation/Qualifiers
                                            /product= "Phytase"
                                                                                        13-AUG-1997; 97US-00910798.
01-WAR-1999; 99US-00259114.
13-APR-1999; 99US-0021931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
                                                                              24-MAY-2001; 2001US-00866379
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/*tag≃ a
                                                                                                                                     GRAY K A.
BARTON N R.
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O' DONOGHUE E
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Д.
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                                                                                                                          (SHOR/) (KRET/) (GRAY/) (GRAY/) (GART/) (GARR/) (GONO/) (MATH/) I
                                                                                                                                                                       Short
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Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.

2003-040002/03

P-PSDB; ADA19446.

Claim 2; Fig 1; 62pp; English

The invention relates to an isolated Escherichia coli polymuclectide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from Wesb. (0.000 Mess). (0.000 Mess) (0.000 Mess). (0.000 Mess) (0.000 Mess). (0.000 Mess) (0.000 Mess). (0.000 Me invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence encodes E. coli B wild-type phytase.

Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;

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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expressing the nucleic acid in a yeast under conditions that allow we expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease is stability at low pH. The phytase enzyme can be used in foodsruffs to improve the feeding value of phytase enzyme can be used in foodsruffs to improve the feeding value of phytase enzyme and fishes, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially significant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as suppy, zebrafish, molly, swordtall, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible incorporated in to the dietary aid is safe for animals. The present sequence is Bscherichia coli B phytase DNA.
                           Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
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WPI; 2004-374952/35
P-PSDB; ADO50292.
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                        PhellealaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
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/note= "Encodes Arg"
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01-MAR-1999; 99US-00259214.
13-APR-1999; 99US-00291331.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00586515.
24-MAY-2001; 2001US-00866379.
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BARTON N R.
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KRETZ K.
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                    541 CGSCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
                                                      LeulyshrgglulysglnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
                                                                                  CTTAAACGTGAGAAACAGGAAGGTGTTCATTAACGCAGGCATTACCATCGGAACTC
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ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                                                 LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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ds; coding sequence; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture; osteoporosis; osteopathic; food.
                                                                             E. coli B phytase coding sequence SEQ ID NO: 1.
                   AEE75412 standard; DNA; 1323 BP
                                                         (first entry)
                                                                                                                                      Escherichia coli B.
                                                         23-FEB-2006
                                       AEE75412;
         RESULT 6
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Location/Qualifiers
1. .1323
/*tag= a
/product= "Phytase"

Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;

40000

Length: Matches: Conservative: Mismatches: Indels:

3.15e-202 2302.00 100.0% 100.0%

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

US-10-601-319-2 (1-440) x AEE75412 (1-1323)

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The present sequence is that of a polymucleotide encoding the Escherichia coli B phytase. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, where the polypeptide is a modified sequence (ARE75412) derived from the cargyme, comprising a series of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition; a kit; an immobilized phytase; a fertilizer or soil additive; a liquid supplement for preventing muscle cramps; a chydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing collution and increasing nutrient availability in an environment or environment sample by degrading environmental phytic acid. The novel caryme is a dietary supplement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The cliquid supplement is useful for preventing muscle cramps. The cliquid supplement or environmental phytic acid, where the environmental sample by degrading environmental phytic caid, where the environment or 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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214. .216
/*tag= b
/note= "ecodes Arg"
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, Zorner P;
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01-MAR-1999; 99US-00259214.
13-ARR-1999; 99US-00291931.
25-MAY-1999; 99US-00318628.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
                                                                                                                                                                          01-SEP-2004; 2004US-00933115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Short JM, Kretz KA, G
Baum W, Robertson DE,
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE B.
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                                                                                       US2005281792-A1
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(GRAY/)
(BART/)
(GARR/)
(ODON/)
(BAUM/)
(ROBE/)
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                                              CAGATGCCTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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1. .1323
/ttag= a
/product= "Mutant phytase enzyme"
214. .216
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/note= "Encodes
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/*tag= c
replace (527,A)
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replace(893,T)
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01-MAR-1999; 99US-00259214.
13-APR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
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replace(895,G)
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P-PSDB; ADO50292, ADO50304.
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BARTON N R.
GARRETT J B.
O'DONOGHUE E.
MATHER E J.
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KRETZ K.
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                                                                                                                                                GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100
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                                                                                                                                                                                                                                           AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140
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                                            PheAlaGlnSerGluProGluLeuLysLeuGluSerValVallleValSerArgHisGly 40
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            TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCACTCGTCATGGT
                                                                                     ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
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                                                                                                                                     ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
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MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla
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Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
                        Disclosure; Page; 74pp; English.
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low ph. The phytase enzyme can be used in foodsatuffs to improve the feeding value of phytase enzyme and fishes, commercially commercially and pathons and and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as plygs, goats, laboratory rodens, commercially significant avian species such as Ghicken, ducks, doves, parrot, etc., of commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish and loading efficiency. The phytase composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present sequence is Escherichia coll w phytase mutant DNA. Note: The present sequence is not shown in the specification but has been derived from the sequence is some of the active index and a phytase composition, and shown in the specification but has been derived from the sequence is some of the active index and a phytase commercially sequence is some of the active index sequence is some of the sequence of the active index sequence is some sequence of the shown in the specification but has been derived from the sequence of the sequ

Sequence 1323 BP; 324 A; 353 C; 356 G; 289 T; 0 U; 1 Other;

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                                                                                                                                                                             AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280
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541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                              CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                                              AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                           GluilePheLeuLeuGinGinAlaGinGiyMetProGluProGiyTrpGiyArgileThr
                                                                                                                                              GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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                                                                               LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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                                  LeulysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
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1. .1323
/*tag= a
/product= "Phytase mu
214 . .216
/*tag= b
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expression of the mucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low ph. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytase right ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant avian species such as pigs, goats, laboratory rodents, commercially significant avian species such as Ghicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtall, ctc., in dough maxing and baxing, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present equence is Kangaroo rat Escherichia coli phytase mutant DNA. Note: The present sequence is the phytase mutant bas been derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
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from Escherichia coli B phytase DNA ADO50291
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/note= "Encodes Arg"
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             13-AUG-1997; 97US-00910798.
01-MAR-1999; 99US-00259214.
13-APR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
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(BART) BARTON N R.
(GARK) GARRETT J B.
(ODON) O'DONGGHUE E.
(MATH) MATHER E J.
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P-PSDB; ADO50302.
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KRETZ K.
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Matches:
Conservative:
Mismatches:
Indels: BP; 325 A; 353 C; 356 G; 288 T; 4.16e-200 2279.00 99.1% 99.1% Percent Similarity: Best Local Similarity: gnment Scores:

US-10-601-319-2 (1-440) x ADO50301 (1-1323)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTCTTCGTTGGCAGGTTTTACGCAA
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                                                                                                                           LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
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Best Local Similarity:
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the foll antiennes sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense conding a polypeptide whose expression is inhibited by the antisense collipseptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of is producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of
                                 CAGATGCGTGATAAAAGGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200
                                                                                                                                                                  LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any one of
GinMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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Xu HH;
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Forsyth RA,
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-WAR-2002; 2002US-0362699P.
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Trawick JD,
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P-PSDB; ABU15427.
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strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target not form prot form the sequence data for this patent did not form part of the printed specification, but was obtained in fit.wipo.int/pub/published_pct_sequences
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The invention relates to recombinant modified Appa phytases having

modified phytase activity. The Appa phytases are derived from a mature

Escherichia coll Appa phytase designated EBC1882 (see AbL16120), and

comprise subsitutions at least one of residues 26, 43, 46, 54, 73, 113,

CC (126, 184, 228, 384 or 410, or at a residue located within 5 residues of

those listed above. The invention also encompasses polymucleotides

c nocding a modified Appa phytase and which further encodes a secretion

signal sequence operable in Bacillus subtiliss) comprising the

colymucleotide sequences; and a method for the production of the modified

Appa phytases. The invention also discloses a method of producing an

c and host calls (preferably Bacillus subtiliss) comprising the

colympetide having phytase activity; a method of producing a heterologous

colympetide having phytase activity; a method of producing a neterologous

colympetide having phytase activity; a method of producing a modified

Appa phytase; and animal feed comprising calls, spores or plant parts,

including seeds, capable of expressing an animal feed additive,

modified Appa phytases are useful as an animal feed additive,

modified Appa phytases are useful as an animal feed additive,

particularly in feeds for non-ruminant livestock such as pigs and poultry

which lack the digestive enzymes for extracting phosphorus from phytate

c modified Appa phytases are useful as an animal feed additive,

particularly in feeds for non-ruminant livestock such as pigs and poultry

which lack the digestive enzymes for extracting phosphorus from phytate

c modifications For example, they can be used in the plant seed which is

an important source of phosphorus. The modified Appa phytases also have

c applications For example, they can be used in the search of the control and mutritional supplements); in wet grain milling; in osteoporosis) and renal calcul (kidney stones); in food products and in the removal products and entented beneval products, and in the removal product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                Novel recombinant phytase having modified phytase activity comprising modification of amino acid residues in mature Escherichia coli phytase designated EBC18B2, useful as feed additive.
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                                                                                                                                                                                                                                                                           Claim 19; Fig 21; 107pp; English
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2004-169498/16.
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                                     P-PSDB; ADL16129
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ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80

121 6 181

ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGCGGTGGTGAGCTAATCGCCTATCTC

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ACGCTTCCCCGGTCAGCCCGGATAACACGCCGCCAGGTGGTGGTGTTTTGAACGCTGG 1080
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GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100
                                                                                                                                      GCCTTCGCCGCCGGCTGGCACCTGTGCAATAACCGTACATACCCAGGCAGATACG 420
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                  GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG
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New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
                                                                         Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; untritional value; feed treatment process; therapy; thermal tolerance; growth performance; alcoholic drink; biopulping; non-alcoholic drink; biobleaching; ds.
                                                                                                                                                                                                                                                                                           0' donoghue
                                                                                                                                                                          /product= "E. coli appA phytase protein"
                                                                                                                                                                                                                                                                                            Garrett JB,
                                                       Escherichia coli appA phytase wild type DNA
                                                                                                                                                                                                                                                                                            Barton NR,
                                                                                                                                           Location/Qualifiers
AAD25463 standard; DNA; 1901 BP
                                                                                                                                                                                                                                                                                                                                                                                Claim 42; Fig 7; 170pp; English.
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                                                                                                                                                                                                                                  24-MAY-2001; 2001WO-US017118.
                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-00580515.
                                                                                                                                                                                                                                                                                           Gray
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                                       entry)
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                                                                                                                                                                                                                                                                                            Short JM, Kretz KA,
                                                                                                                                                                                                                                                                         (DIVE-) DIVERSA CORP
                                      (first
                                                                                                                                                                                                                                                                                                             WPI; 2002-083108/11.
P-PSDB; AAE15807.
                                                                                                                          Escherichia coli.
                                                                                                                                                                                             WO200190333-A2
                                      26-MAR-2002
                                                                                                                                                                                                               29-NOV-2001
                   AAD25463;
                                                                                                                                              Key
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The patent discloses recombinant bacterial phytase from Escherichia coli (12 apph phytase. The enzyme has phytase activity and improved thermal tolerance when compared with wild-type phytase. It has improved protease stability at low ph. The recombinant phytase is useful for improving the mutritional value of phytate-containing foodsruffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are producing or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of environmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed. The present sequence is a DNA encoding E. coli appA phytase wild type protein

U; 1 Other; 499 G; 428 T; 0 BP; 474 A; 499 C; 1901 Sequence

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1901
430
0
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                      Conservative:
Mismatches:
Indels:
Gaps:
       Length:
Matches:
       7.83e-196
2235.00
99.5%
99.5%
                               Similarity:
                       Percent Similarity
Alignment Scores:
Pred. No.:
                                Best Local Si
Query Match:
DB:
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(1-1901)x AAD25463 US-10-601-319-2 (1-440)

> 12 RESULT

1387

420

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1388 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCCATGTTTCGTTGGCAGGTTTTACGCAA 1447
                                                                                                                                                                                                                                                                                                     Phytase; ds; gene; phytate; appA gene; animal feed; inorganic phosphate; digestion enhancement; transgenic; thermal tolerance; protease stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated Bscherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from W688, Q84W, A95P, K97C, S168E, R180Y, N22G or Y277D. Also included the E. coli appA gene ADA19449 (or an oligonucleotide derived from it) or its mutant sequence ADA19452, expression vectors,
GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                           CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                  LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barton NR, Garrett
                                                                                                                                               ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1483
                                                                                                                                 IleValAsnGluAlaArgIleProAlaCysSerLeu 432
                                                                                                                                                                                                                                                                             E. coli K12 appA gene encoding phytase.
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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01-WAR-1999; 99US-00259114.
13-APR-1999; 99US-0021931.
25-WAY-1999; 99US-00318528.
25-WAY-2000; 2000US-00580515.
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O' DONOGHUE B.
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containing foodstuff by contacting the phytate-containing foodstuff with containing foodstuff by contacting the phytate-containing foodstuff with a pure bibytase enzyme mutated bipytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in the phytate. Containing foodstuff, a method to produce an animal feed containing a microbial phytase (comprising culturing the plant cell, plant part or plant under conditions where the nucleotide sequence is expressed and converting the plant cells, plants or plant into a composition for animal converting the plant seeds, plant cells, plant parts or plants in admixture with a phytate-containing converting the plant cells, plant parts or plants in admixture with a phytase enzymes codistiff, a method to treat a human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzymes comprising administering to the human or animal the plant seed, plant cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence contain an expression system which expresses a nucleotide sequence comprising a heterologous nucleic acid sequence encoding a polypeptide having phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence represents the E. coli KI2 appA gene encoding wild-type phytase.
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Sequence 1901 BP; 474 A; 499 C; 499 G; 428 T; 0 U; 1 Other;

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 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses a new isolated or recombinant nucleic acid which encodes a polypeptide having a phytase activity. Also claimed is a nucleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, a nanisense oligonucleotide, inhibiting the translation of a phytase message in a cell, a heterodimer comprising the polypeptide and a second domain, an array comprising immobilised polypeptide or nucleic a phytase message in a cell, a heterodimer comprising the polypeptide and a second domain, an array comprising immobilised polypeptide or nucleic a second domain, an array comprising a granule edible enzyme delivery cartix, an edible pellet comprising a granule edible carrier and the polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, thermotolerance or thermoetability of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a digestive system and processing of corn and sorghum kernels. The phytase cativity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in hyptate digestion. The sequence presented is the DNA case an aid in phytate digestion. The sequence presented is the DNA
                                                                                                                                                                                                                                                                                                                                        * nucleic acid encoding a polypeptide having phytase activity, useful
improving the feeding value of phytate rich ingredients or as an aid
phytate digestion.
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01-MAR-1999; 99US-00259214.
13-APR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00586515.
24-MAY-2001; 2001US-00866379.
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                                                         ACCTGGCCGGTAAAACTGGGGTTGGCTGACACCGCGNGGTGGTGGCTAATCGCCTATCTC
                                                                                                                              GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to inmprove the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fools and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially significant avian species such as chicken, ducks, doves, parrot, etc.,
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/*tag= a
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401. .403
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                                                                                                                                          Escherichia coli K12 appA phytase DNA
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/note= "Encodes Arg"
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99US-00259214.
99US-0021931.
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BARTON N R.
GARRETT J B.
O'DONOGHUE E.
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KRETZ K.
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25-MAY-2000;
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commercially farmed fish such as guppy, zebrafish, molly, swordtail, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is asfe for animals. The present sequence is Escherichia coli K12 apph phytase DNA.
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Matches:
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Scoring table:

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15 AY496073
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Location/Qualifiers
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TITLE
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                                                                                                                   June 14, 2006, 10:58:44; Search time 5255.78 Seconds (without alignments) 8030.264 Million cell updates/sec
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                GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                - nucleic search, using frame_plus_p2n model
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                GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro
                                                       GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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Short, J.M. and Kretz, K.A.
Recombinant bacterial phytases and
Patent: US 6183740-A 1 06-FEB-2001;
Location/Qualifiers
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Kretz, K.
Phytase
Patent: US 6190897-A
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patent US 6190897.
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Sequence 1 from patent
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180 220 120 240 100 300 120 360 140 420 160 480 180 540 200 900 240 720 260 780 99 9 20 9 40 80 41 ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCCAGACGATGGCCA GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro GGACATTACCAAGGCAGGGTCTGGTAGCCGACGGATTGCTGCTGGCGAAAAAGGGCTGCCCG ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys GluilePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgileThr GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 1323 440 0 0 0 Length:
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261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280

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Bacherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Unclassified.
1 (bases 1 to 1323)
Short, J.M., Kretz, K.A., Gray, K.A., Barton, N.R., Garrett, J.B., O'Donoghue, B. and Marhur, B.J.
O'Donoghue, B. and Marhur, B.J.
Patent: US 6855365-A 1 15-FEB-2005,
Diversa Corporation; San Diego, CA
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Sequence 1 from patent US 6855365.
AR636185
AR636185.1 GI:62768868

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Enterobacteriaceae, Escherichia.
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ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAgpLeuIleMetAlaAla
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Location/Qualifiers
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Enterobacteriaceae, Escherichia.
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                                                                                                                                               Short,J.M., Kretz,K.A., Gray,K.A., Barton,N.R., O'Donoghue,E.
Recombinant bacterial phytases and uses thereof Patent: WO 0190333-A 7 29-NOV-2001;
DIVERSA CORPORATION (US)
Location/Qualifiers
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                                                                                            AlapheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr
                                                                                                             SerSerProAgpProLeuPheAgnProLeuLysThrGlyValCysGlnLeuAspAgnAla
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NYDAILSRAGGSTADFTGATAPTPALERVINPPGSNLCLKREKQDESCSLTQALPS

SLLKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF

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188. . 253

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Ostanin, K. and Van Etten, R.L.
Asp304 of Escherichia coli acid phosphatase is involved in leaving
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Etten,R.L.
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J. Biol. Chem. 267 (32), 22830-22836 (1992)
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1811 ATGAAAGCCATCTTAATCCCATTTTTATCTCTGATTCCGTTAACCCCGCAATCTGCA 1870
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                                                                                                   Forsberg, C.W., Golovan, S. and Phillips, J.P.
Transgenic animals expressing salivary proteins
Patent: WO 0064247-A 4 02-NOV-2000;
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                                  GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
                                                                                                                                         TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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Best Local Similarity: 99.5% Mismatches: 2 Query Match: 97.1% Indels: 0 DB: 2 Gaps: 0 US-10-601-319-2 (1-440) x AX042373 (1-6708)	Qy 1 MetLysalaileLeuileProPheLeuSerLeuileProLeuihrProGinSerala 20	Qy 21 PheAlaGlnSerGluProGluLeuLySLeuGluSerValValIleValSerArgHisGly 40	Qy 41 ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	Qy 61 ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80	QY 81 GlyHisTyrGlnArgGlnArgCcnArgCcnAr	Qy 101 GINSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120	Oy 121 AlabhealaalaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140	Oy 141 SerSerProAspProLeuBheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160	Qy 161 ASNVALThrASDAlaIleLeuSerArgAlaGlyGlySerIleAlaAsDPheThrGlyHis 180	Qy 181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200	Oy 201 LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220	Qy 221 LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	Qy 241 GluilePheLeuLeuGlnGlnalaGlnGlyMetProGlyTrpGlyArgileThr 260	Qy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280 	Qy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla 300	Qy 301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320	Phellealagl TTTATCGCCGG
Db 2411 CTTAAACGTGAGAAACGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 2470 Qy 221 LygValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240 Db 2471 AAGGTGAGCGCGACAATGTCTCATTAACCGGTAGGTAAGCCTCGCATCAATGCTGACG 2530	Qy 241 GlullePheLeuLeuGlnGlnalaGlnGlyMetProGlyTrpGlyArglleThr 260 	Qy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280 	Qy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla 300 	Qy 301 LeuThrProHisBroProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320 	Oy 321 PheilealaglyHisaspThrasnLeualaasnLeuglyGlyAlaLeugluLeuasnTrp 340	Qy 341 ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp 360	Qy 361 ArgArgLeuSerAspAsnSerGlnTrp11eGlnValSerLeuValPheGlnThrLeuGln 380 11	Qy 381 GlnMetArgAsplysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400	Qy 401 LeualagiyCysGluGluargasnalaginGlyWetCysSerLeualaglyPheThrGln 420	Qy 421 IleValAsnGluAlaArgIleProAlaCysSerLeu 432 	RESULT 15 AX042373 LOCUS AX042373 6708 bp DNA linear PAT 23-NOV-2000 DEFINITION Sequence 2 from Patent W00064247,		SOURCE synchetic construct ORGANISM synthetic construct REFERENCE 1	Forsberg, Transgeni Patent: W	FEATURES Location/Qualiflers source 1. 6708 /organism="synthetic construct" /mol_type="unassigned_DNA"		Alignment Scores: 1.72e-197 Length: 6708 Pred. No.: 2235.00 Marches: 430 Percent Similarity: 99.5% Conservative: 0

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        Qy
        341 ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluargTrp
        360

        Db
        2831 AcGCTTCCCGGTCAGCCGGATAACAGCCCAGGTGGAACTGGTTTTGAACGCTGG
        2890

        Qy
        361 ArgAsqLeuPacAgCCGAGTAACAGCCCAGGTGGATTTGAACGCTGG
        2890

        Qy
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        2950

        Qy
        381 GlmMctArgAspLysThrProLeuSerLeuAsmThrProProGlyGluValLysLeuThr
        400

        Db
        2951 CAGATGCTGATAAAAACGCCGTGCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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        Qy
        401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMctCysSerLeuAlaGlyPheThrGln
        420

        Db
        3011 CTGGCAGGATGTGAATGCGCAGGGCATGTTCGTTGGTAGCAGGTTTTACGCAA
        3070

        Qy
        421 IleValAanGluAlaArg1leProAlaCysSerLeu
        432

        Db
        3071 ATCGTGAATGAACGCGATTTGCTTCGTTGGTAGGTATTACGAA
        3070
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Search completed: June 14, 2006, 13:53:05 Job time: 5289.78 secs

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OM protein - protein search, using sw model

June 13, 2006, 10:22:24; Search time 25.7339 Seconds (without alignments) 1645.118 Million cell updates/sec Run on:

US-10-601-319-2 2302 1 MKAILIPPLSLLIPLTPQSA......IVNEARIPACSLRSHHHHHH 440 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		å			SUMMARIES	
Result No.	Score	Query	Query Match Length	B B	ID	Description
п	2235	97.1	432	~	B36733	acid phosphatase (
7	2210	96.0	434	~	H90770	phosphoanhydride p
m	2210	96.0	444	N	D85633	ш
4	943.5	41.0	441	~	AC0201	
2	545	23.7	413	7	F90773	periplasmic glucos
9	545	23.7	413	~	B85636	
7	541	23.5	417	7	S25627	glucose-1-phosphat
80	539	23.4	413	~	JV0087	glucose-1-phosphat
0	526	22.8	414	~	E87316	periplasmic phosph
10	524	22.8	413	~	AG0632	glucose-1-phosphat
11	139.5	6.1	423	Н	806167	acid phosphatase (
12	133	5.8	416	N	T16058	hypothetical prote
13	131	5.7	423	7	A33395	phosphat
14	122.5	5.3	421	N	S14742	
15	117	5.1	386	٦	JH0610	
16	113.5	4.9	344	0	B89130	protein F52E1.8 [1
17	109	4.7	2554	-	TVFF7L	kinase-related pro
18	108.5	4.7	10223	7	T30225	Bynt
19	107.5		457	~	A56925	
20	107	•	450	7	A54429	
21	106.5	4.6	1048	-	BVECSC	exonuclease (EC 3.
22	105.5	4.6	459	~	852250	paired box transcr
23	104.5	4.5	2535	7	AC0304	probable hemolysin
24	102	4.4	638	N	A29440	signal recognition
25	101.5	4.4	397	~	C81716	hypothetical prote
56	101.5	4.4	479	-	JN0890	acid phosphatase (
27	•	4.4	524	~	H75530	probable acid-CoA
28	101.5	4.4	1047	0	C85535	ATP-dependent dsDN
53	101.5	4.4	1047	0	G90684	

	tenascin-A - bovin pilin glycosylatio hypothetical prote exonuclease SbcC [malate oxidoreduct hypothetical prote
T18540 138344 JQ2278 S64682 S58315 AG2897 A97673 A83572 VCBB17	142829 (81983 D83186 AB0551 H75256 T32457
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0 1 2 2 4 2 2 4 2 4 2 4 2 4 2 4 2 4 2 4 2	1 4 4 4 4 4 5 4 4 6 6 7

ALIGNMENTS

RESULT 1 B36733 acid phosphatase (EC 3.1.3.2) precursor - Escherichia coli (strain K-12) N.Alternate names: phosphoshbydride phosphoshodrolase nesthlasmic: phosps
Cispecias: Bacherichia coli Cispecias: Bacherichia coli Cibate: 19-Apr-1991 #sequence revision 19-Apr-1991 #text change 09-Jul-2004 CiAccession: B36733; S18018; E64839; A26534; S17960; S33278
R;Dassa, J.; Marck, C.; Boquet, P.L. J. Bacteriol. 172, 5497-5500, 1990 A;Title: The complete nucleotide sequence of the Escherichia coli gene appA reveals sign
A;Reference number: A36733; MUID:90368616; PMID:2168385 A;Accession: B36733

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-432 c.DAS>
A;Cross-references: UNIPROT: P07102; UNIPARC: UPI000004750A; GB:M58708; NID:g145283; PIDN
R;Greiner, R.; Jany, K.D.
Biol. Chem. Hoppe-Seyler 372, 664-665, 1991
A;Title: Characterization of a phytase from Escherichia coli.

A; Accession: S18018

A; Molecule type: protein A; Residues: 23-33 <GRE>

A;Cross-references: UNIPARC;UP10000179815
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A;Molecule type: DNA A;Residues: 1-43. SBLATA A;Crose-references: UNIPARC;UPI000004750A; GB:AE000200; GB:U00096; NID:g2367111; PIDN:AA A;Experimental source: strain K-12, substrain MG1655

RiTowati, E.; Danchin, A.
Biochimie 69, 215-221, 1987
Aritile: The structure of the promoter and amino terminal region of the pH 2.5 acid phos A.Reference number: A26534; WUID:87271766; PMID:3038201
A;Accession: A26534

A; Molecule type: DNA A; Residues: 1-50, NAGCHPRRMANLAG', 65, 'T', 67-74,' DV', 77-111,'S' <TOU> A; Cross-references: UNIPARC: UP1000016EDE2; GB:X05471; NID:g40925; PIDN:CAA29031.1; PID:g A; Cross-references: UNIPARC: UP1000016EDE2; GB:X05471; NID:g40925; PIDN:CAA29031.1; PID:g R; Dassa, J.; Feihi, H.; Marck, C.; Dion, M.; Kieffer-Bontemps, M.; Boquet, P.L. Mol. Gen. 229, 341-352, 1991 Mol. Gen. Genet. 229, 341-352, 1991 A; Title: A new oxygen-regulated operon in Escherichia coli comprises the genes for a put A; Reference number: S17958; MUID:92049231; PMID:1658595

A;Cross-references: UNIPARC:UP1000016FFB1; GB:S63811; NID:g238656; PIDN:AAB20286.1; PID: A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-17 <- DA2>

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119 GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT 178
                                                                                  Query Match
Best Local Similarity 98.4%;
Matches 427; Conservative
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                                                                                                                                                                                                                                                                                                                       A. Man Desition: 25 min
C. Keywords: monomer; periplasmic space; phosphohistidine; phosphoprotein; phosphoric
F;1-22-50 fomain: signal sequence #status predicted <8IG>
F;23-112/Product: acid phosphatase #status predicted <MAT>
F;38/Active site: Arg #status predicted
F;39/Active site: His (phosphohistidine intermediate) #status predicted
R;Greiner, R.; Konietzny, U.; Jany, K.D.

Arch. Blochem. Blophys. 303, 107-113, 1990
A;Title: Purification and characterization of two phytases from Escherichia coli.
A;Reference number: S33278; MUD:93256556; PMID:8387749
A;Accession: S33278
A;Accession: S33278
A;Accession: S33-34
A;Residues: 23-31,'A',33-34 <GR2>
A;Residues: 23-31,'A',33-34
Cxosa-references: UNIPARC:UPI0000179816
C;Comment: In addition to cAMP-mediated control, this enzyme is induced when bact naerobic conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
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99.5%;
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Best Local Similarity
Matches 430; Conserv
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: D85633
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85633
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPRCT:Q8XC29; UNIPARC:UP10000165751; GB:AE005174; NID:g12514245; PN
A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                             MKAILIPPLSLLIPLTPQSAFAQSEPEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDA
                                                                                                                                                                                                                                                           61 WPNWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLTKKGCPQPGQVAIIADVDERTRKT
                                                                                                                                                                                                                                                                                                                                                                    RWRRLSDNSQWIQVSLVPQTLQQWRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGF
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                                                                                                           1 MKAILIPFLSLLIPLTPQSAFAQS--BPELKLESVVIVSRHGVRAPTKATQLMQDVTPDA
                                                                                                                                                                                                                      59 WPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKT
                                                                                                                                                                                                                                                                                                                                    GEAFAAGLAPDCAITVHIQADISSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT
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  Length 434;
                                                         Indels
Score 2210; DB 2;
Pred. No. 1.2e-169;
0; Mismatches 5;
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A;Accession: F90773
A;Accession: F90773
A;Status: preliminary
A;Status: preliminary
A;Actession: F90773
A;Actession: Preliminary
A;Cross-references: UNIPROT:Q8XBZ6; UNIPARC:UPI00000D0533; GB:BA000007; PIDN:BAB34581.1;
A;Genetics:
A;Gene: EC91158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Escherichia coli
C)Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85636
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
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                          366 ELWQNPDNHQRYYAVKMPYQTMDQLRNAEKLDLKANPAGIISVAVAGCENNGDDKLCELD 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MP--EPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 FPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL-----
      ERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSL-NTPPGEVKLTLAGCEERNAQGMCSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 PRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 IPLIPQSAFAQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAWPTWPVKLGWLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.7%; Score 545; DB 2; Length 413; 32.1%; Pred. No. 6.1e-36; Live 76; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periplasmic glucose-1-phosphatase (imported) - Escherichia coli
                                                                       417 GFTQIVNEARIPACSL 432
                                                                                             | : | : | | : TPQKKVAKVIEPACHI 441
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Matches 135; Conservative
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acid phosphatase (BC 3.1.3.2) [imported] - Yersinia pestis (strain CO92)
Species Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0201
B.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Cillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitchead, S.; Barrell, A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0201
A;Accession: AC0201
A;Estius: Preliminary
A;Molecule type: DNA
A;Residues: 1-441 <KURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q8ZFP6; UNIPARC:UPI0000DCCF7; GB:AL590842; PIDN:CAC90470.1; Genetics:
A,Gene: YPO1648
C;Keywords: phosphoric monoester hydrolase
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LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM 298
                                                                                                                                                                                                                                                                                       430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 IFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAAL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHRQTAFRELERVLNFPQSNLCLNREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM
                                                                                                                                        LTEIFLLQQAQGMPEPGMGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM
                                                                                                                                                                                                       311 IALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVPE
                                                    GHRQTAFRELERVINFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM
                                                                                                                                                                                  AALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFE
                                                                                                                                                                                                                                                    RWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGF
                                                                                                                                                                                                                                                                     5 LIPPLSLIPLIPQSAFAQSEPE-LKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWP
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Best Local Similarity 45.6%;
Matches 199; Conservative 6
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                                                                                                                                                                                                                                                                                                                    TOIVNEARIPACSL 432
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69 72 DCAITVHTQADISSPOPLFNPLKTGVCQLDNANVIDAILSRAGGSIADFTG--HRQTAFR 186 133 GCKVNIHHOPEIGKMDPVFNPIIT-----NGSPEFKOKALAAMDDYLKGLSLKAGYE 184

129

70 TPRGGELIAYLGHYORQRLVADGLLAKKGCPOSGO-VALIADVDERTRKTGEAFAAGLAP

10 SLLIPLIPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWL

185 ELDTVIAIKDSQKC----KTDKLCNLDSQKNSFIIEADKEPGVSGPLKIANSAVDAIDLQ 240

ELERVIANFPOSNICLKREKODESCSLTQALPSELKVSADNVSLTGAVSLASMLTEI FLLQ

187

247 QAQGMP--EPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPH 304

305 PPOKQAYGVTLPTSVLFIAGHDTNLANLGGALELN-WTLPGQPDNTPPGGELVFERWRRL 363

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Local Similarity 30.5%; Pred. No. 1.3e-35; es 129; Conservative 84; Mismatches 182;
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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Fitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Recession: B85636
A;Status: preliminary
A;Residues: 1-413 csTO>
A;Residues: 1-413 csTO>
A;Cross-references: UNIPROT:Q8XEZ6; UNIPARC:UPI00000D0533; GB:AE005174; NID:g12514273; E
A;Gene: agp
                                                                                                                                                                                                                                                                                                                                                                  187 IVNYKDSPAC----KEKQQCSLVDGKNTFSAKYQQEPGVSGPLKVGNSLVDAFTLQYYEG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VIDRISAPKITVLVGHDSNIASLLIALDFKPYQLHDQNEKTPIGGKIVFQRWRDSK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 ANRDLMKIEYVYQSAEQLRNADALTLQAPAQRVTLELSGC-PIDADGFCPMDKFDSVLNE 410
                                                                                                                                                                                                                                                                                                                                              PRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAGLAPDC 130
                                                                                                                                                                                                                                                                                                                                                                                                            131 AITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MP--EPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQK 308
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                                                                                                                                                                                                                                                                                                   VLNPPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 FPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL----
                                                                                                                                                                                                                                                                                13 IPLIPQSAFAQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAWPTWPVKLGWLT
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                 Length 413;
                                                                                                                                                                                                                 23.7%; Score 545; DB 2; Length 41:
32.1%; Pred. No. 6.1e-36;
tive 76; Mismatches 180; Indels
                                                                                                                                                                                                                                Best Local Similarity 32.13
Matches 135, Conservative
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Glucose-1-phosphatase (EC 3.1.3.10) precursor - Providencia rettgeri
C;Species: Species: S
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CiKeywords: periplasmic space; phosphohistidine; phosphoprotein; phosphoric monoester F1-29/Domain: signal sequence #status predicted <SIGS / SIGS / SIGN +
DB 2; Length 417;

23.5%; Score 541;

Query Match

F;314/Active site: His #status predicted

PIDI

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glucose-1-phosphatase (EC 3.1.3.10) precursor - Escherichia coli (strain K-12) C;Species: Escherichia coli (c)Species: Escherichia coli (c)Species: Bacherichia coli (c)Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: JV0087; H64841 B. Hards, C.; Boquet, P.L. J. Bacteriol: 172, 802-807, 1990 A;Fitle: Nucleotide sequence and transcriptional analysis of the Escherichia coli agp ger A;Reference number: JV0087; MUID:90130318; PMID:2153660
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-413 - CRAA.
A; Residues: 1-413 - CRAA.
A; Cross-references: UNIPROT: P19926; UNIPARC: UPI00001256FB; GB: M33807; NID: G145217; PIDN: R;
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coll
A, Rose, D.J.; Mau, B.; Shao, Y.
Science J7, 1453-1462, 1997
A; Rieterence number: A64720; MUID: 97426617; PMID: 9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UDI00001256FB; GB:AE000202; GB:U00096; NID:g1787233; PIDN:AAC
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Description: essential for growth in a high-phosphate medium containing glucose-1-phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Note: optimal at low pH
C;Keywords: homodimer; periplasmic space; phosphohistidine; phosphoprotein; phosphoric mc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;2-3-413/Product: glucose-1-phosphatase #status predicted <MAT>
F;40/Active site: His (phosphohistidine intermediate) #status predicted
F;311/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: H64841
A;Status: nucleic acid sequence not shown, translation not shown
A;Molecule type: DM
A;Residues: 1-413 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: agp
A;Map position: 23 min
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Glucose-1-phosphatase precursor (GlPase), secreted [imported] - Salmonella enterica subsidiacies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: Ad0632
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wair, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP10000059FE6; GB:AL513382; PIDN:CAD08242.1; PID:g16502289;
C;Genetics:
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                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                            WRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFT 419
                                                                                                                                                                                                                                                                                                                                                                            80 LGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQAD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGHYTREWLVAQGLIPSGECPAPDTVYAYANSLQRTVATAQFFITSAFPGCDIPVHHQEK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                          177 EQLDALLMQCDKGPCPPAPGKRRVFDAKPGFVDG--EEL-----AGLSGPEAFASGVTE
                                                                                                                 IFILOQAQGMPEPGWG-RITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
                                                                                                                                                                                                                                                             | |---KEKHQCSLIDAKDTFSANYQQEPGVQGPLKVGNSLVDAFTLQYYEGFPMDQVAWG
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                                                                                                                                                                                                                             LIPHPPOKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG-QPDNTPPGGELVFER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 AQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAWPTWPVKLGWLTPRGGELIAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 AQTTPEGYQLQQVLMMSRHNLRAPLANNGNVLAQSTPNAWPAWDVPGGQLTTKGGVLEVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
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B87316

periphasmic phosphoanhydride phosphohydrolase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87316
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87316
A;Scatus: prellminary
A;Molecule type: DNA
A;Residues: 1-414 <STO>
A;Crossion: E6700
A;Crossion: E6700
A;Crossion: Ferences: UNIPROT:Q9AQ4; UNIPARC:UPI00000C70A0; GB:AE005673; NID:g13421731; F
C;Genetics:
A;Gene: CC0542
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                                                                                                                                                                                                                                                                                                                                      AITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRBLER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MP--EPGWGRITDSHOWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAF 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 PPMDQVAMGEIKSDQQMKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL-----
                                                                                                                                              71 PRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDC
                                                                                                                                                                                                                                                       | :: |:|: |:|: |:|: |:|: |:| | | | | |:| | ::| | | |:| | |:| | |:| | |:| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| |::| | |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  VINFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEI FLLQQAQG
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                                                          Gaps
                                                             30;
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     Length 413;
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23.4%; Score 539; DB 2; Length 41 32.1%; Pred. No. 1.8e-35; ive 75; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%; Score 526; DB 2; Length 41 34.7%; Pred. No. 2.1e-34; rive 57; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 34.78
Matches 148; Conservative
                                                       Conservative
                          Local Similarity
nes 135; Conserv
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  Query Match
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A;Cross-references: UNIPROT:Q19390; UNIPARC:UPI000007AD42; EMBL:U40939; NID:g1072175; PII
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                                                                               ----A 429
                                                                                                                                                                                                                                                    328 YF---RNESDKAPWPLSLP-----GCPHR-----CPLODFLRL-TEPVVPKDWQQE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGA 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 VSLASMLTEI---FLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 ATPLLD----LIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQ 345
                                 LPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSL 374
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A;Introns: 23/3; 59/3; 88/3; 138/3; 202/3; 244/1; 270/3; 312/3; 349/3; 377/1
C;Superfamily: mammalian acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSI
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                                                                                                                                                                                 375 VFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyaccession: T16658
RiFulton, L.
Submitted to the EMBL Data Library, November 1995
A; Reference number: S69020
A; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F13D11.1 - Caenorhabditis elegans
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A;Cross-references: UNIPARC:UP10000131FE1; EMBL:X12548; NID:g34262; PIDN:CAA31064.1; PID
A;Note: part of this sequence, including the amino end of the mature protein, was confit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P11117; UNIPARC:UP10000131FB1; EMBL:X15525; NID:g34239; PIDN R;Geier, C.; von Figura, K.; Pohlmann, R. Br. J. Biochem. 183, 611-616, 1989
A;Title: Structure of the human lysosomal acid phosphatase gene.
A;Reference number: S05525; MUID:89377828; PMID:2776754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-29 <GEI>
A;Cross-references: UNIPARC:UPIO0001727CD
A;Pohlmann, R.; Krentler, C.; Schmidt, B.; Schroeder, W.; Lorkowski, G.; Culley, J.; Mer
EMBO J. 7, 2343-2350, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Human lysosomal acid phosphatase: cloning, expression and chromosomal assignmer
A;Reference number: S01155; MUID:89052645; PMID:3191910
A;Accession: S01155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 PWASPQTMQRLSRLKDFSFRFLFGIYQQAEKARLQGGVLLAQIRKNLTLMATTSQ---- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 FNP-LKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------DRLLKFPLGPCPRYEOL 165
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                                                                                                                                                                                                           NiAlternate names: acid phosphatase, lysosomal
Cispecies: Homo sapiens (man)
Cibate: 04-Dec-1992 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004
CiAccession: S06167; S05525; S01155
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QSARQLRNAEALTLKSPAQRVTLELKGCPV-DANGFCPLDKFDNVMNTA 411
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                                                                                                                                                                                 phosphatase (EC 3.1.3.2) ACP2 precursor [validated] - human
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6.1%; Score 139.5; DB 1; Length 4
Best Local Similarity 23.1%; Pred. No. 0.0023;
Matches 98; Conservative 44; Mismatches 180; Indels
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                                                                                                                                                                                                                                                                                                                                                      R;von Figura, K.
submitted to the EMBL Data Library, June 1989
A;Reference number: $06167
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A; Residues: 1-423 < VON>
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A;Gene: GDB:ACP2
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A;Molecule type: DNA
A;Residues: 1-386 <SHA>
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acid phosphatase (BC 3.1.3.2) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan.1990 #sequence_revision 29-Jan.1990 #text_change 09-Jul-2004
C;Accession: A33395
R;Himeno, M.; Fujita, H.; Noguchi, Y.; Kono, A.; Kato, K.
Biochem: Biophys. Res Commun. 162, 1044-1053, 1989
A;Title: Isolation and sequencing of a cDNA clone encoding acid phosphatase in rat liver
A;Reference number: A33395; MUD:89350910; PMID:2764916
A;Reference number: A33395
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-423 <HIM>A;Residues: 1-423 <HIM>A;Residues: 1-423 <HIM>A;Residues: 1-423 <HIM>A;Cross references: UNIPROT:P20611; UNIPARC:UPI0000131FEZ; GB:M27893; NID:g202933; PIDN:C;Superfamily: mammalian acid phosphatase
C;Superfamily: mammalian acid phosphoprotein; phosphoric monoester hydrolase
C;Superfamily: site: Arg #status predicted
F;42/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 EKWPQGPGQLTKEGMLQHWELGQALRQRY--HGFL---NASYHRQEVYVRSTDFDRTLMS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHRQTAFRELERVINFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 LTEIPL------LQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF-YLLQRTPEVA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 RSR-----ATPLLDLIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 WTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NGKQAPYASCHIFELYQ--EDNGNF-SVEMYFRNDSK----FD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 LANLTLETIWAVYDTLFCEQTHGLLLPPW---ASPQTVQALSQLKDFSFLFLFGIHDQVQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
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                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 131; DB 2; Length 423;
22.8%; Pred. No. 0.011;
tive 49; Mismatches 184; Indels 122;
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A,Accession: S14742
A,Status: preliminary
A,Modecule type: mRNA
A,Modecule type: mRNA
A,Reses: 1-421 cGE1>
A,Cross-references: UNIPROT: P24638; UNIPARC: UPI0000027103; EMBL: X57199; NID: G52870; PIDN C,Superfamily: mammalian acid phosphatase
C,Superfamily: mammalian acid phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                    phosphatase
acid phosphatase (EC 3.1.3.2) precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S1474.
R;Gelar, C.; von Figura, R.; Pohlmann, R.
Biol. Chem. Hoppe-Seyler 372, 301-304, 1991
A;Telle: Molecular cloning of the mouse lysosomal acid phosphata
A;Reference number: S14742; MUID:91282986; PMID:2059337
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146
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                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                        54 YQEEKWPQGFGQLIKEGMLQHWELGQALRQRY--HGFL---NTSYHRQEVYVRSIDFDRI 108
                                                                                                                                                                                                                                                                                                          116 RKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIA 175
                                                                                                                                                                                                                                                                                                                                                                                                           176 DFTGHROTAFRELERVINFPOSNLCLKREKODESCSLTOALPSELKVSADNVSLTGAVSL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSRATPLLDLIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 NGKQAPYASCHIPELYQ--EDNGNF-SVEMYPRNDSK---KAPWPLILP------GC 343
                                                                                                                                                          53
                                                                                                                                     DAWPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVD-ERT
                                                                                                                                                                                                                                                                                                                                                         109 LMSARANLAGLFPP-----NEVQHFSPNISWQPI-----PVHTVPITE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DRLLKFPLGPCPRYEQLONE----TRQTPEYQNRSIQNAQFLNMVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 ASMLTEIFL-----LQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 ETGLTNVTLETIWNVYDTLFCEQTHGLLLPPWASPQTVQRLSQLKDFSFLFLFGIHEQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 KARLOGGVLLAQILKNLTLMATTSQP-----PKLLVYSAHDTTLVALQMALNVY----
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                                                                                                      2 KAILIPF----LSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTP
                                                         Indels 107;
     ; Score 122.5; DB 2;
; Pred. No. 0.054;
49; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EERNAQGMCSLAGFTQIVNEARIP 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHR-----CPLODFLRL-TEPVIP 361
cn 5.3%;
l Similarity 21.8%;
97; Conservative 49
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     Query Match
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                            Best Local
Matches 9
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NiAlternate names: acid phosphatase, prostatic; orthophosphoric monoester phosphohydrola C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Speci acid phosphatase (EC 3.1.3.2) ACPP precursor [validated] - human

A;Cross-references: UNIPROT:P15309; UNIPARC:UP10000039832; GB:M97580; GB:M97581; GB:M975 A;Accession: USG693 A;Molecule type: mRNA A;Residues: 1-386 <SH3>

A;Cross-references: UNIPARC:UP10000039832; GB:M97589; NID:g189611; PIDN:AAA60021.1; PID:: R;Van Etten, R.L.; Davidson, R.; Stevis, P.E.; MacArthur, H.; Moore, D.L. Davidson, Chem. 266, 2313-2319, 1991 A;Title: Covalent structure, disulfide bonding, and identification of reactive surface a A;Reference number: A38608; MUID:91115848; PMID:1989985

A; Molecule type: mRNA A; Accession: A38608

A; Residues: 1-386 <VAN>

Ajcross-references: UNIPARC:UP10000039832; GB:M34840; NID:g189620; PIDN:AAA69694.1; PID: Ajcross-references: UNIPARC:UP10000039832; GB:M34840; NID:g189620; PIDN:AAA69694.1; PID: Ajchock: part of this sequence, including the amino end of the mature protein, was confir. R;Vihko, P.; Virkkunen, P.; Henttu, P.; Roiko, K.; Solin, T.; Huhtala, M.L. FEBS Lett. 236, 275-281, 1988
FEBS Lett. 236, 275-281, 1988
Ajtitle: Molecular cloning and sequence analysis of cDNA encoding human prostatic acid pi A;Reference number: S01331; MUID:88312981; PMID:2842184
Ajacession: S01331

A;Molecule type: mRNA A;Residues: 1-14,'A',16,'ASC',20,'CF',23,'C',25-65,'WIWPTHPA',74-211,'A',213-386 <VIH> A;Cross-references: UNIPARC:UP1000016A48C; EMBL:X52174; NID:g28321; PIDN:CAA36422.1; PID

15;

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113
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A; Note: part of this sequence, including the amino end of the mature protein, was confir R; Sharief, F.S.; Lee, H.; Leuderman, M.M.; Lundwall, A.; Deaven, L.L.; Lee, C.; Li, S.S. Biochem. Biophys. Res. Commun. 160, 79-86, 1989
A; Title: Human prostatic acid phosphatase: CDNA cloning, gene mapping and protein sequen A; Reference number: A32419; MUD:89228054; PMID:2712834
A; Reference number: A32419
A; Rolecule type: mRNA
A; Residues: 1-14, A*, 16, ASC', 20, CF', 23, 'C', 25-94, 'D', 96-115, 'R', 117-214, 'S', 216-293, 'T A; Cross-references: UNIPARC:UPT000016AE62; GB:M24902; NID:9189618; PIDN:AA460022.1; PID: A; Note: the authors translated the codons GAC for residue 95 as Glu, CGT for residue 116
B; Tailor, P. G.; Govindan, N.V.; Patel, P.C.
A; Tailor, P. G.; Govindan, N.V.; Patel, P.C.
A; Tetle: Nucleotide sequence of human prostatic acid phosphatase determined from a full-Appear: S11147; MUID:90370491; PMID:2395659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S11147
A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Rolecus: 1-14, 'AFASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RIWPTHPA', 74-138, 'E', 140-156, 'R
A;Cross-references: UNIPARC: UPI000016APIA; EMBL: X53605; NID: G35683; PIDN: CAA37673.1; PIE
R;Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.
B;Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.
A;Description: Characterization of the promoter of the human prostatic acid phosphatase
A;Reference number: S38863
A;Accession: S38863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-40 < LABAN>
A; Residues: 1-40 < LABAN>
A; Residues: 1-40 < LABAN>
A; Crossidues: 1-40 < LABAN
A; Crossidues: 1-40 < LABAN
B; Virkkunen, P.H.; Hedberg, P.; Palvino, J.J.; Birr, E.; Porvari, K.; Taavitsainen, P.; submitted to the EMBL Data Library, September 1993
A; Description: Structural organization of human and rat prostate-specific acid phosphata equence in the human gene promoter.
A; Reference number: 841251
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A;Cross-references: UNIPARC:UPI0000039832; EMBL:U07097; NID:G515995; PIDN:AAB60640.1; PI
C;Gomment: This protein is synthesized under androgen regulation by epithelial cells of
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Cross-references: GDB:119644; OMIM:171790
A.Cross-references: GDB:119644; OMIM:171790
A.Map position: 3421.3-3425.2
A;Introns: 40/3; 72/3; 10/3; 122/3; 185/3; 216/3; 260/3; 288/3; 323/2
C;Function:
A.Description: catalyzes the hydrolysis of a wide range of phosphate esters
C;Superfamily: mammalian acid phosphatase
C;Keywords: Glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
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A; Residues: 1-40 <VIRS
A; Cross-teferences: UNIPARC: UP10000006BB; EMBL: X74961; NID: 9439657; PIDN: CAA52913.1; 1
A; Lee, H.; Chu, T.M.; Li, S.S.L.; Lee, C.
B; Lee, H.; Chu, T.M.; T.; 759-765, 1991
B; A; Liel: Homodimer and heterodimer subunits of human prostate acid phosphatase.
A; Title: Homodimer and heterodimer subunits of human prostate acid phosphatase.
A; Reference number: S17042; MUID: 9133699; PMID: 1908222
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A.Residues: 1-40 - RAZ>
A.Cross-references: UNIPARC:UPI0000006BB; GB:X71391; NID:g416530; PIDN:CAA50514.1; ER; Sharief, F.S.; Li, S.S.
Biochem: Mol. Biol. Int. 33, 561-565, 1994
A.Title: Nucleotide sequence of human prostatic acid phosphatase ACPP gene.
A.Reference number: 137175; MUID:95038536; PMID:7951074
A.Accession: 137175; MUID:95038536; PMID:7951074
A.Retaus: preliminary; translated from GB/EMBL/DDBJ
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R;Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.
Biochim. Biophys. Acta 1217, 188-194, 1994
A;Title: Analysis of the promoter of the human prostatic acid phosphatase gene. A;Reference number: S42730; MUID:94153995; PMID:8110833
A;Accession: S42730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 PIKESSWPQGFGQLTQLGMEQHYELGEYIRKRY-----RKFLNESYKHEQVYIRSTDV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 SIADFIGHRQTAFRELERVINFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGA 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 EVARSRATPLLDLIMAALTPHPPOKOAYGVTLPTSVLFIAGHDTNLANLGGALEL-NWTL 342
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-386/Product: acid phosphatase ACPP #status experimental <MAT>
F;43,86/Active site: Arg #status predicted
F;44/Active site: His (phospholistidine intermediate) #status predicted
F;94/Active site: Garbohydrate (Asn) (covalent) #status experim
F;161-372,215-313,347-351/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                       Query Match 5.1%; Score 117; DB 1; Length 386; Best Local Similarity 19.8%; Pred. No. 0.13; Matches 87; Conservative 63; Mismatches 178; Indels 112;
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ORGANISM: Sue scrofa
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TYPE: PRT
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Sequence 34904, A
Sequence 34902, A
Sequence 56, Appl
Sequence 224, Ap
Sequence 8296, Ap
Sequence 8296, Ap
Sequence 2758, Ap
Sequence 2758, Ap
Sequence 2564, Ap
Sequence 2564, Ap
Sequence 2123, Ap
Sequence 2123, Ap
Sequence 2125, Ap
Sequence 2125, Ap
Sequence 2125, Ap
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551.244 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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               GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-293-697-2264
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US-11-293-697-3256
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US-11-293-697-3256
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US-10-953-349-7
US-11-293-697-3134
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ALIGNMENTS

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US-11-270-040-6

US-11-270-040-6

SEQUENCE OF US20060110762A1

SEQUENCE TITLE OF INVENTION: SYNDOMEN VIRE RECEPTOR COMPONENTS AND USES THEREOF

TITLE OF INVENTION: SYNDOMEN USES US 11/270,040

TITLE OF INVENTION: SYNDOMEN USES US 11/270,040

CURRENT PELICATION NUMBER: 60/626,788

PRIOR APPLICATION NUMBER: 60/626,788

PRIOR PRIOR PRIOR PRIOR NUMBER: 60/626,788

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US-10-953-349-34902

US-10-953-349-34902

Sequence 34902, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE PEPERENCE: 2790-1579910S

CURRENT PELICATION NUMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SEQ ID NO 34902

LENGTH: 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 DCEASIDLPSDDLRPYLRVAYD-----AAPADKLSAI--LQBPR--PERPDWVLIDYA 126
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                                                                                                                                                                                                                                                                      170 AGGSIADFT-----GHRQTAF---RELERVLNFPQS------NLCLKR-EKQDE 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 HOWNTLLSLHNAOFYLLORIPEVARSRATP--LLDLIMAALIPH--PPQ----KQAYGVT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 KPEDLITVVPDYVPFPTTVAHRGFEAREL--FKPGLVPDDSGVSEGHRFGVSIGESQIVGI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 RSKTELESEWLÓV-----LGKLYKKPVIPIGLFPPP--PTODIACHEATLRWLDROAGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 SCSLTQALPSE----LKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPE-PGWGRITDS 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AYW--------APAAARHGVPCAFLSLFGAATLSFYGPFEGLMGRGKYART 162
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1 Similarity 25.1%; Pred. No. 0.39;
81; Conservative 37; Mismatches 107; Indels 98;
                                                                                                                                                                     ch 4.2%; Score 97; DB 6; Length 464; 11 Similarity 25.1%; Pred. No. 0.38; 81; Conservative 37; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 MCSLAGFTQIVNEARIPACSLRS 434
                                                                       ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34903
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SOFTWARE: Patentin version 3.3 SEQ ID NO 34903
LENGTH: 464
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
ITILE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION WUMBER: US/10/953,349
CURRENT APPLICATION WUMBER: US/10/953,349
CURRENT APPLICATION WUMBER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 275-1579-1953
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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---ASPNALRVDMEEL 1604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 VARSRATPLLDLIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG 344
                                                                                                345 QPDNTP-----PGGELVPERWRRLSDNSQWIQVSLVPQTLQQMRDKTPLSLNTPPGEV 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQWNTLLSLHNAQFYLLQRTPEVARSRATP--LLDLIMAALTPH--PPQ----KQAYGVŢ 314
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25.1%; Pred. No. 0.38;
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                                                                                                                                              RVDSEPLASLTLHLGSRLVASSQPQAAPAKPHIRVS
                                                                                                                                                                                                                                            1605 KPSDQGEYVCSASNALGSASAATY 1628
                                                                                                                                                                                               398 KLTLAG---CEERNAQGMCSLAGF 418
                                                                                                                                                                                                                                                                                                                                                          Sequence 34904, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVVYAAFG---SEAKLTSAQLQT 288
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US-10-953-349-34904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.19
Matches 81, Conservative
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4.0%; Score 91.5; DB 6; Length 635;
Best Local Similarity 19.8%; Pred. No. 1.9;
Matches 111; Conservative 65; Mismatches 196; Indels 189;
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##PELICANT: MOITLE, MECLOLIALS
##PELICANT: MOSTILE, Steven
### TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
### TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
### TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
### TITLE OF INVENTION: UNUABER: US/10/511,937
### CURRENT APPLICATION NUMBER: PCT/US2003/012946
### PRIOR PELLING DATE: 2003-04-24
### PRIOR FILING DATE: 2003-04-24
### PRIOR PELLING DATE: 2003-04-24
### PRIOR PELLING DATE: 2003-04-24
### PRIOR PELLING DATE: 2003-04-24
### PRIOR FILING DATE: 2003-13-20
### NUMBER OF SEQ ID NOS: 3117
### SOPTWARE: PatentIn Version 3.2
### SSG ID NO 2424
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                                                                                                                        3793 NEELYLGGYPDYGAIPKAGLSSGFIGCVRELRI 3825
                                                                                398 -- KLTLAGCEERNAQGMCSL-AGFTQIVNEARI
                                                                                                                                                                                                                                                                                                                  Sequence 2424, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
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Prentice, James
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; ORGANISM: Homo sapiens
US-10-511-937-2424
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APPLICANT:
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APPLICANT: Wanderbilt University
APPLICANT: Wanderbilt University
APPLICANT: Wanderbilt University
APPLICANT: Wallahan, Dennis E
APPLICANT: Wallahan, Dennis E
APPLICANT: Wallahan, Dennis E
CURRENT PULLIS OF INVENTION: IN VUMBER: US/11/183,325
CURRENT PILLING DATE: 2005-07-13
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR PILLING DATE: 2001-10-03
PRIOR PILLING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.3
SEQ ID NO 56
LENGTH: 4391
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171 KPEDLTVVPDYVPPPTTVAHRGFEAREL--FKPGLVPDDSGVSEGHRFGVSIGESQIVGI 228
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4.1%; Score 93.5; DB 7; Length 4391;
Best Local Similarity 21.4%; Pred. No. 21;
Matches 110; Conservative 50; Mismatches 186; Indels 167;
                                                                 360 WRRLSDNSQWIQVSLVPQTLQQMRDK--TPLSLNTPPGEVKLTLAGCE---
                                                                                                                                                                                                                                                    281 SVVYAAFG---SEAKLTSAQLQT 300
                                                                                                                                                                                                     412 MCSLAGFTQIVNEARIPACSLRS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/11183325 Publication No. US20060104898A1 GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: P98160
DATABASE ENTRY DATE: 2003-02-28
RELEVANT RESIDUES: (1)..(4391)
US-11-183-325-56
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Sequence 8255, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
ENCORNES - DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:
FILE REPERRICE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:
CURRENT FILING DATE:
SOFTWARE: PATENTION NOS: 40252
SOFTWARE: PATENTION NOS: 40252
                                                       372 SGSPNGLLSDIK-----FRWMNLTFRRWSNYSAGLVDYRPGCQGLVNHRATSGIIMEHVN 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 GFRVENVDLK-WSDDDDVNAAMNVPLEFRPSTVNNVSFVGFTS--GLYTKLFESDXVMSL 483
                       140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADF-----TGHRQTAFRELERVL 192
                                                                                                                          NFPQSNLCLKREKQDESCSLTQALPSELKVS-ADNVSLTGAVSLASMLTEIFLLQQAQGM 251
                                                                                                                                                                       426 GFRVENVDLK-WSDDDVNAAWNVPLEPRPSTVNNVSFVGFTS--GLYTKLFESDYVMSL 482
                                                                                                                                                                                                                         252 PEPGWGRITDSHOWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADF-----TGHRQTAFRELERVL 192
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                                                                                                                                                                                                                                                                                                                              312 GVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDN------TPPGGELVFERW 360
                                                                                                                                                                                                                                                                                                                                                                              511 -KTLRNRIHFRSGSTSTGPS-----RWATPGHEERPKGYFMNRTPPPPGGSRKWEDW 561
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                                                                                                                                                                                                                                                                         ---ESEIGITKMASTKPLIVAA----
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4.0%; Score 91; DB 6; Length 614;
Best Local Similarity 20.9%; Pred. No. 2;
Matches 50; Conservative 31; Mismatches 92; Indels
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; Publication No. US20060105376A1
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA; PILE REPERENCE: H.-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR PILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5588
; SOFTWARE: PatentIn Ver. 2.1
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484 -----FTSNHQYIT-----
                                                                                                                                                                                                                                                                              ----FTSNHQYIT----
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 8297
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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|-----FISNHQYIT------355
                                                                            140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADF-----TGHRQTAFRELERVL 192
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                                                  ----KLTLAGCEER 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KTLRNRIHFRSGSTSTGPS-----RWATPGHEERPKGYFMNRTPPPPGGSRKWEDW 406
----LSAVLGLLLLRWQFPAHYRRLRHALWPSLPDLHRVLGQYLRDTAALSPPKA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 4.0%; Score 91; DB 6; Length 458; I Similarity 20.9%; Pred. No. 1.3; 50; Conservative 31; Mismatches 92; Indele
                                               359 RWRRLSDNSQWIQVSLVPQTLQQMRDKTPLSLNTPPGEV----
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                                                                                                                                                                                                                                                                                                                         ; Sequence 8297, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                  408 NAQGMCSLAGFTQIVNEARIP 428
                                                                                                                                                                                 611 AESGSCCT---THIANHSYLP 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8297
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US-10-953-349-8296
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Matches 50; Conservative
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Best Local Similarity
Matches 50; Conserva
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US-10-953-349-8297
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1094 -QVAQNVALYTG-----DPNL----GLEL------PEAAGDIFFDGAWER--- 1127
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                                    --PGWGRITDSHQWNTLLSLHNAQFYLLQRT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AF-----PLFNPLKTGVCQLD 158
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                                                                      |:: | | | | : : | | | 407 VSVMEBERFLLEAMEGPPELYIPDMACAKTTTRGECPRKDSHLWQ-LLPMPHAEY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GWLTPRGGELIAYLGHYQ--RQRLVA----DGLLAKKGCPQSGQVAIIADVDERTRKTGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Mismatches 163; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Ly, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Morris, MacDonald
APPLICANT: Morris, Morris, Monitons FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 5066-12000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR PLING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR PLING DATE: 2002-04-24
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21.4%; Pred. No.
                                                                                                                                                  PEVARSRATPLLDLIMAALTPHPPQKQ
                                                                                                                                                                                                                                                                                                                                                     Sequence 2564, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
                                 236 ASMLTEIFLLQQAQGMPE-
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Best Local Similarity 21.44
Matches 99; Conservative
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SOFTWARE: Patentin version
SEQ ID NO 2564
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                                                                                                                                                                                                                                                                                                                                                                                                                           118 VWLLSRAEVRPRSALGSSRRGLGDKGPRSRRAÅEFTQARPTRKRRTPGGGRPEAG--CWL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 LIPELPTQISSSRPTRPRRCKSSSRPHL-----ARGRRSPLKAAQ--ODRGLPAWG 117
                                                                                                                                                                                                                                                                                                                                                                             61 TWPVKLGWLTPRG--GELIAYLGHY-QRQRLVADGLLAKK------GCPQSGQVAII 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAGGSIADFTGHRQTAFRELERVIANFPQSNLCLKREKQDE----SCSLTQALPSELKVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKK------GCPQSGQVAIIADVDERTRK------TGEAFAAGLAPDCAI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 SKOWPCSSMPAKQAPPSCVSEG----SVKGRTQKENLPQTNKLKSLSRLAGKGPD--- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 SFEMBEVQSPERETGNPLDM-----TSGTVGARVDRANSCQSDSSGFLEEPLFPLPLQM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 INFPGSNLCLK---REKQDESCSLTQALPSELK-------VSADNVSLTGAVSL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 FSSLLSDVSILPNRAEEKAGGESVQRTSVSAAKEHRRRMGKLLRRASK-QNIRRDCNPEV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 SESFKVKDEVFVPFTKPWDCGARLAATSINHKQNHLSLSVEHQSLQACDDLLPYPPHGLL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 TVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELE-RV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 FLSLL--IPLTPQSAFAQSEPE-LKLESVVIVSRHG-----VRAPTKATQLMQDVTPDA 58
                                                                                                                                                                                                         88; Gaps
                                                                                                                                                                                                                                                         5 LIPPLSLLI----PLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----OWRLLPRRPERAAGSAGSCSSRRALPA----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 3.8%; Score 87.5; DB 7; Length 952; Local Similarity 21.7%; Pred. No. 7.8; nes 84; Conservative 50; Mismatches 144; Indels 109;
                                                                                                                                            ch 3.9%; Score 90; DB 7; Length 384; I Similarity 24.2%; Pred. No. 1.2; 66; Conservative 24; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 ADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGW 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 GSGAAMTGSWA-------APPRPAW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVESTION: Novel full length CDNA TITLE OF INVESTION: Novel full length CDNA FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
RIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3284, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-293-697-3284
                                                                                                                                         Query Match
Best Local Similarity
Matches 66; Conserv
                                                                               US-11-293-697-2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-11-293-697-3284
LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
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Best Local &
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Sequence 22123, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: BROONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22123
LENGTH: 360
                        295 DLIMAALTPHPPQKQAYGVTLPTSVL 320
                                                                 298 DPEQMLPSPSPP---SFSPPAPTSVL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2...
SEQ ID NO 3258
LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-293-697-3258
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ORGANISM: Glycine max
                                                                                                                                                                       RESULT 14
US-11-293-697-3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C340
CURRENT PELLING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: U0/05286
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 PQALAT-----RALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDADEWVKARNQHG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 LASMLTBIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 PDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDA----ILSRAGGS--IADFTGHR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 QTAFRELERVINFPQSNLCLKREKQDESCS----LITQALPSELKVSADNVSL-TGAVS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
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                               366 NSQWIQVSLVFQTLQQMRDKT-PLSLNTPPGEVKLTLAGCEE 406
                                                                                                                                                                                             Sequence 350, Application US/10196749 Publication No. US20060094864A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Goddard, Audrey
                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo Sapien
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169 QLVIER-------LQGEKEQKENSELSTGLMDSEMTPTIEGCVKDVSYQGG 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GHRQTAPRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 QH--TVNTELEKQIS------NEVDSE------DLKWSSEVKHICGEDQIEDK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 LTEIFLLQQAQGMPEPGWGRITD----SHQWNTLLSLHNAQFYLLQRTPEVARSRATPL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 M-------ETVIENIEVVTHQ----ITVQQEQLQLLEE-PETVVSRE--- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- SLCPEE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 ELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGC-EERNAQGM 412
-----IRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPE-----LS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 LDLIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 GQESTPGIVPD-AVQVHTEEQQXS----HPSES----LD----TDSLL-----IAVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 CSL-----AGFTQI-----VNEARIPACSLRSHHHHHH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 KSIKLSSETESSFSSADISKADVSSSPTPSSDLPSHDMLHN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ESRPPKLVMESVTLPLETL-VSPHEESI----
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3.6%; Score 84; DB 7;
Best Local Similarity 19.9%; Pred. No. 11;
Matches 68; Conservative 52; Mismatches 93
                                                                                                                                                                                                                                                                                                                        Sequence 3258, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT PILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
253
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18;

US-10-953-349-22123

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85 RORLVADGLLAKKGCPQSGQVAIIADVDERT---RKTGEAFAAGLAPDCAITVHTQADTS 141
                                                                                                                                                                  142 SPDPLFNPLKTGVCQLD-NANVTDAILSRAGGSIADFTGHRQTAFRELERVLNPPQSNLC 200
                                                                                                                                                                                                                                                                                         201 LKREKQDESCSLTQALPSELKVSADNVSL----TGAVSLASMLTEIFLLQQAQGMPEPGW 256
                                                                                                                                                                                                                                                                                                                | | : |: : | : |: |: | 1.20 -----DLSPASQQSVAGQASKSGNDVLLDLLSIGSPSVESSSSTVDILSSNSSNKAP-- 201
                                                                                                                                                                                                                                                                                                                                                               257 GRITDSHQWNTLLSLANAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAYGVTLP 316
                                                                                                                                                                                                                                                                                                                                                                                         202 ---VSSLDGLSSLSLSTK-----TTSNAAPMMDL-LDGFAPIPPTEN-NGPVYP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                     317 TSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 SVTAFES-----SSLRLTFNFSKQPGN--PQTTVIQATFMNLSSNT---YTDFVF 290
                                                                                            34 VIVSRHGVRAPTKATOLMODVTPDAWPTWPVKLGWLTPRGGE-----LIAYLGHY----O
                                         Gaps
Query Match 3.6%; Score 82.5; DB 6; Length 360; Best Local Similarity 21.1%; Pred. No. 5.4; Matches 82; Conservative 53; Mismatches 155; Indels 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 QT----LQQMRDKTPLSLNTPPGEVKLT 400
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1 MKAILIPFLSLLIPLTPQSA......IVNEARIPACSLRSHHHHH 440 US-10-601-319-2 2302 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 seqs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Post-processing: Minimum DB Maximum DB

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp1980s:* geneseqp1990s:* Genesed 8: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

Aab37892 Escherich Aae12836 Escherich Aae15806 Escherich Ada1946 E. coli B Ado50292 Escherich Aeb50302 Escherich Ado50302 Kangaroo Aab3625 Lama2/APP Aab3625 R15/APPA Aab3625 R15/APPA Aab3626 Escherich Ada19450 E. coli K Abu15427 Protein e Ad67745 Escherich Ad16129 Escherich SUMMARIES AEE75413 ADO50304 ADO50302 AAB36257 AAB36261 AAB36262 AAB36259 AAB36259 AAB36258 AAB36263 ABP53625 ADA19450 ADC87745 ADL16129 ADO50298 AAB37892 AAE22836 AAE15806 ADA19446 ADO50292 AAU77775 AAE15807 8808 Length DB Query Match 1 100.0 100.0 100.0 99.1 2235 2235 2235 2235 2235 2235 2235 Result Š

Aed50820 Escherich	Aee75419 E. coli B	Aef15220 Escherich	Aae02631 E. coli a	Adl16131 Shigella	Aae02634 E. coli a	Adl16130 Shigella	Aae02635 E. coli a	Aay94753 E. coli a		Aae02632 E. coli a	Ad102198 AppA. 5/2	Abr42162 Escherich	Aay01513 An Escher	Adc87743 Modified	Aef15219 Escherich	Adw76361 Phytase A	Ado50300 Escherich	Aed50818 Escherich	Aee75421 E. coli B	Aae15808 Escherich	Adal9451 E. coli K
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24	52	26	27	28	29	30	31	32	33	34	35	36	37 21	38	39	40 21	41	42	43	44	45

ALIGNMENTS

Escherichia coli B; phytase enzyme; anabolic; phytate digestion; AAB37892 standard; protein; 440 AA Escherichia coli B phytase enzyme. 25-MAY-2000; 2000WO-US014846 99US-00318528 (first entry) (DIVE-) DIVERSA CORP. Short JM, Kretz KA; WPI; 2001-112081/12. N-PSDB; AAC88885. Escherichia colf. WO200071728-A1. 25-MAY-1999; 07-MAR-2001 30-NOV-2000 nutrition AAB37892; AAB37892

Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from Claim 1; Fig 1; 147pp; English. the phytates.

The present sequence is a phytase enzyme from Bscherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate in phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients

Sequence 440 AA;

Gaps ö Query Match 100.0%; Score 2302; DB 4; Length 440; Best Local Similarity 100.0%; Pred. No. 2.7e-223; Matches 440; Conservative 0; Mismatches 0; Indels 0

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                                                                                                RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
              LTPHPPOKOAYGVTLPTSVLP1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVPERW
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                                                                                                                                                                        EI FLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
 MKAILIPPLSLLIPLTPQSAPAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dietary aid; biocompatible composition; therapeutic; digestive tract; foodstuff; digestion; phytase; enzyme.
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biocompatible composition is effective upon oral consumption and release in the digestive tract of a subject. The dietary aids are useful for delivering enzymes, therapeutics, medicine and agents to an organism. The use of enzymes and other agents in digestive aids of livestock or domesticated animals not only improves the animal's health and life expectancy but also assists in increasing the health of livestock or the production of foodstuffs from livestock. The present sequence is
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(first entry)

20-NOV-2003

ADA19446;

E. coli B phytase.

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The patent discloses recombinant bacterial phytase from Escherichia colicity appA phytase. The enzyme has phytase activity and improved thermal colerance when compared with wild-type phytase. It has improved protease stability at low ph. The recombinant phytase. It has improved protease stability at low ph. The recombinant phytase is useful for improving the nutritional value of phytate-containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are also used for generating recombinant digestive system life forms, for producting or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of enzionmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral cupplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed.

The present sequence is B. coll B phytase protein
                                                                                                                                                                               New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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                                                         O' donoghue
                                                         Garrett JB,
                                                      Gray KA, Barton NR,
                                                                                                                                                                                                                                                                                       Claim 1, Fig 1, 170pp, English.
  (DIVE-) DIVERSA CORP.
                                                      Kretz KA,
                                                                                                        WPI; 2002-083108/11.
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TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
                                                                                                                              AFAAGLAFDCAITVHTQADTSSPDFLFNFLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
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Claim 1; Fig 1; 62pp; English

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Phytase; enzyme; phytate; appA gene; animal feed; inorganic phosphate; digestion enhancement; transgenic; thermal tolerance; protease stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garrett JB
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                                                                                                                                            /note= "Encoded by CGN"
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 digestion in humans and animals.
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                                                                                                                                                                                                                                                                                                         97US-00910798.
99US-00259214.
99US-00291931.
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25-MAY-2000; 2000US-00580515
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KRETZ K A.
GRAY K A.
BARTON N R.
                                                             Escherichia coli B.
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The invention relates to an isolated Escherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from WEBE. Q84W, A95P, K97C, S168E, R180Y, N25C or Y277D.

Also included the E. coli appa gene ADA1949 (or an oligonucleotide derived from it) or its mutant sequence ADA1945; expression vectors, containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutacted phytase (where the phytase enzyme catalyzes containing foodstuff), a method to produce an animal feed containing a microbial phytase (comprising culturing the plant cell, plant part or converting the plant cells, plants or plant into a composition for animal (converting the plant cells, plants or plants or plant into a composition for animals (comprising the plant cells, plant parts or plants in admixture with a phytate-containing foodstuff), a method to ranimals (comprising to the animal the plant seed, plant cells, plant parts or plants in admixture with a phytate-containing foodstuff), a method to treat a human or an animal the plant seed, plant cells, plant parts or plants of a transgenic plant whose genome contain an expression system which expresses a nucleotide sequence containing a phytase enzyme, a transgenic non-human organism whose genome comprising a hytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The

ADA19446 standard; protein; 440 AA

ADA19446 ID ADA1 RESULT 4

I VNEAR I PACSLRSHHHHH

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LTPHPPOKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
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  24-MAY-2001; 2001US-00866379.
                                      GRAY K A.
BARTON N R.
GARRETT J B.
O'DONOGHUE E
                                                                                                                             WPI; 2004-374952/35.
                                                                                                Kretz K,
                                                                             MATHER E J
                    SHORT J N
KRETZ K.
                                                                                                                                       N-PSDB; ADO50291
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 440 AA;
                                                                                                Short JM,
Mather EJ;
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                                                                                                                                       TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
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                                                                                                                                                                                                                                                                          EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300
                                                                                                                                                                                                                                                                                               LIPHPPQKQAYGVILPISVLFIAGHDINLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
                                                                                                                  9
invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence represents E. coli B wild-type phytase.
                                                                                                             TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
                                                                                                                                                                                       AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
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                                                                                                 1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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                                                                             Gaps
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                                                          Length 440;
                                                                             0; Indels
                                                        100.0%; Score 2302; DB 6;
100.0%; Pred. No. 2.7e-223;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli B phytase enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                       ADO50292 standard; protein; 440
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99US-00259214.
99US-00291931.
99US-00318528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                             Matches 440; Conservative
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                                                                    Best Local Similarity
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                                         Sequence 440 AA;
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low ph! The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as suppy, zebrafish, molly, swordtall, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present sequence is Escherichia coli B phytase enzyme.
                                                                                                                                                                                                                                           Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
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O'donoghue E;
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    Garrett JB,
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Barton NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 2; 74pp; English.
    Gray KA,
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29-JUL-2004
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                                                                                                                                                     enzyme; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture; osteoporosis; osteopathic; food.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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                                                                                                                                                                                                                           /note= "Encoded by CGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2; 82pp; English.
                                                                                                                                                                                                       Location/Qualifiers
                                                                     AEE75413 standard; protein; 440 AA
                                                                                                                                E. coli B phytase SEQ ID NO: 2.
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, Zorner
421 IVNEARIPACSLRSHHHHHH
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99US-00259214.
99US-00291931.
99US-00318528.
2000US-00580515.
                                                                                                                                                                                                                                                                                     01-SEP-2004; 2004US-00933115
                                                                                                             (first entry)
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Baum W, Robertson DE,
                                                                                                                                                                                                                                                                                                                                                                                                 GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
BAUM W.
ROBERTSON D E
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                                                                                                                                                                                  Escherichia coli B.
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KRETZ K A.
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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                                                                                        AEE75413;
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bone loss, and preventing muscle cramps. The liquid supplement is useful for preventing muscle cramps. The method is useful for reducing pollution and increasing nutrient availability in an environment or environmental sample by degrading environmental phytic acid, where the environment environment comprises a soil or a body of water. The immobilized phytase is useful in foodstuffs for improving the feeding value of
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                                                                                                                                                                                                                                                        Length 440;
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                                                                                                                                                                                                                                                                                                      Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "E. coli B phytase Asp replaced
                                                                                                                                                                                                                                                   Score 2302; DB 10;
Pred. No. 2.7e-223;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli W phytase 875PH2 mutant enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Encoded by CGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Misc-difference 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO50304 standard; protein; 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVNEAR I PACSLRSHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVNEAR I PACSLRSHHHHH
                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 440; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                   phytate rich ingredients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 299
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 160
                                                                                                                                                                                                    Sequence 440 AA;
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360

420

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301 LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
                                                                                                                                                                                                   361 RRLSDNSQWIQVSLVPQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420
181 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
                                                                                                          LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                             RRLSDNSQWIQVSLVPQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O' donoghue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "E. coli B phytase Asp replaced with Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "E. coli B phytase Gly replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kangaroo rat Escherichia coli phytase 872PH1 mutant enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garrett JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "E. coli B phytase Met replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barton NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by CGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             ADO50302 standard; protein; 440 AA.
                                                                                                                                                                                                                                                                          IVNEARIPACSLRSHHHHHH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00910798.
99US-00259214.
99US-00291931.
99US-00318528.
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24-MAY-2001; 2001US-00866379
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRAY K A.
BARTON N R.
GARRETT J B.
O'DONOGHUE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kretz K,
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N-PSDB; ADO50301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 176
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KRETZ K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 72
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13-APR-1999;
25-MAY-1999;
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(BART/)
(GARR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme in the yeast. The invention also relates to modified phytase enzyme can be used in foodsurifs to improve the feeding value of phytase enzyme can be used in foodsurifs to improve the feeding value of phytase rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant ammals such as pigs, goats, laboratory rodents, commercially significant avian species such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present sequence is Becherichia coli W phytase mutant enzyme. Note: The present sequence is Becherichia coli W phytase mutant enzyme. Note: The present sequence is not shown in the specification but has been derived from Escherichia coli B phytase ADOSO292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
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                                                                                                                                                                                                                                                                                                                                                                                               Garrett JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%; Score 2282; DB 8;
99.1%; Pred. No. 2.9e-221;
ive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                               Barton NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page; 74pp; English.
                                                                                                                         13-AUG-1997; 97US-00910798.
01-WAR-1999; 99US-00252214.
13-APR-1999; 99US-00291931.
25-WAY-1999; 99US-00318528.
25-WAY-2000; 2000US-00586515.
24-WAY-2001; 2001US-00866379.
                                                                                                                                                                                                                                                                                                                                                                                               Gray KA,
                                                                                         20-JUN-2003; 2003US-00601319
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-374952/35.
N-PSDB; ADO50291, ADO50303.
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                                                                                                                                                                                                                                                                                   (GRAY) GRAY K A.
(BART) BARTON N R.
(GARK) CARRETT J B.
(ODON/) O'DONOGHUE E.
(MATH/) MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                               Kretz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    SHORT J M.
KRETZ K.
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                      JS2004091968-A1
                                                      13-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                               Short JM,
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                                                                                                                                                                                                                                                                      KRET/)
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원 ò g ઠે Lama2/APPA plasmid translated sequence.

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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow cappression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pit. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme and fishes, commercially commercial including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially significant mammals such as pigs, goats, laboratory rodents, commercially farmed fish such as guppy, zebrafish, molly, swordtail, significant avian species such as chicken, ducks, doves, parrot, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase composition, higher yields and loading efficiency. The present sequence is Rangaroo rat Escherichia coli phytase mutant enzyme. Note:

The present sequence is not shown in the specification but has been constructed from Escherichia coli B phytase sequence ADOS0292.
Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
                                                                                                                         Disclosure; Page; 74pp; English
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Sequence 440 AA;

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                                                                                1 MKAILIPPLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCERNAQGMCSLAGFTQ
                                                              1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATOLMODVTPDAWP
                                                                                                                          TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
                                                                                                                                           AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
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                                 Gaps
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Length 440;
                              4; Indels
99.0%; Score 2279; DB 8; 99.1%; Pred. No. 5.7e-221; ive 0; Mismatches 4;
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              Best Local Similarity 99.1
Matches 436; Conservative
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Query Match
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                  Transgenic animal; salivary protein; phytase; phosphorus; animal growth; environmental pollution; pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides transgenic animals which produce desired
                                                                                                                                                                                                                                                                                                                                                                             expression of a protein, preferably phytase, comprises a nucleic acid sequence including a heterologous transgene construct encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKAILIPPLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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Pred. No. 1.6e-216;
0; Mismatches 2;
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99.5%;
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Best Local Similarity 99.5
Matches 430; Conservative
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                                                                                       Escherichia coli
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                                                                                                     Chimeric.
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420

RELSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ

361

AAB36257 standard; protein; 432 AA

RESULT 9

(revised)
(first entry)

12-SEP-2003 20-FEB-2001 AAB36257;

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181 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
                              EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic animal; salivary protein; phytase; phosphorus; animal growth;
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99.5%; Pred. No. 1.6e-216;
iive 0; Mismatches 2;
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(first entry)
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Matches 430; Conservative
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Escherichia coli
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20-FEB-2001
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Pred. No. 1.6e-216;
0; Mismatches 2;
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                                                                                                    AAB36261 standard; protein; 432 AA.
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                Matches 430; Conservative
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 IVNEARIPACSL
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N-PSDB; AAC68298.
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Best Local Similarity
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Escherichia coli.
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              proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the E. coli APPA phytase coding sequence. (Upp on 12-SEP-2003 to standardise OS field)
 present invention provides transgenic animals which produce
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Pred. No. 1.6e-216;
0; Mismatches 2;
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Matches 430; Conservative
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Escherichia coli
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               TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
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12-SEP-2003 20-FEB-2001

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RESULT 12 AAB36259

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Pred. No. 1.6e-216;
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97.1%; Score 2235; D
Best Local Similarity 99.5%; Pred. No. 1.6e
Matches 430; Conservative 0; Mismatches
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                                                                                                                               R15/APPA plasmid translated sequence.
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                                    AAB36260 standard; protein; 432 AA.
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N-PSDB; AAC68297.
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Escherichia coli.
Chimeric.
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earch completed: June 13, 2006, 10:22:03 ob time : 141.266 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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June 13, 2006, 10:17:34; Search time 192.752 Seconds (without alignments) 2111.554 Million cell updates/sec - protein search, using sw model OM protein Run on:

2302 1 MKAILIPPLSLLIPLTPQSA.....IVNEARIPACSLRSHHHHHH 440 US-10-601-319-2 Perfect score:

BLOSUM62 Scoring table: Sequence:

2849598 segs, 925015592 residues Searched:

Gapop 10.0 , Gapext 0.5

2849598 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-112.
MEDLINE=87271766; PubMed=3038201; DOI=10.1016/0300-9084(87)90045-9;
Touati E., Danchin A.;
"The structure of the promoter and amino terminal region of the pH 2.5 acid phosphatase structural gene (appA) of E. coli: a negative control of transcription mediated by cyclic AMP.";
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MEDLINE-97426617; PubMed-9278503; DOI-10.1126/science.277.5331.1453;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Rigor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIRAIN=KALS, MEDLINE=90368616; PubMed=2168385; MEDLINE=90368616; PubMed=2168385; Marck C., Boquet P.L.; The complete nucleotide sequence of the Escherichia coli gene appAreveals significant homology between pH 2.5 acid phosphatase and
                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Escherichia.
                                                                                                                                                                       Periplasmic appA protein precursor [Includes: Phosphoanhydride phosphohydrolase (EC 3.1.3.2) (pH 2.5 acid phosphatase) (AP); 4-phytase (EC 3.1.3.26) NamesappA; OrderedLocusNames=b0980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                            01-APR-1988, integrated into UniProtKB/Swiss-Prot. 01-AUG-1991, sequence version 2. 07-MAR-2006, entry version 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-K12 / MG1655;
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   432 AA
PRT;
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J. Bacteriol. 172:5497-5500(1990)
   STANDARD;
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PPA_ECOLI
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                                                 "A new oxygen-regulated operon in Escherichia coli comprises the genes for a putative third cytochrome oxidase and for pH 2.5 acid phosphatase (appA).";
Mol. Gen. Genet. 229:341-352(1991).
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MEDLINE=20122624; PubMed=10655611; DOI=10.1038/72371;
Lim D., Golovan S., Forsberg C.W., Jia Z.;
"Crystal structures of Escherichia coli phytase and its complex with phytate.";
Nat. Struct. Biol. 7:108-113(2000).
-!-CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND PROTEIN SEQUENCE OF 23-35.
MEDIJNE-923-56556; PubMed=8387749; DOI=10.1006/abbi.1993.1261;
Greiner R., Konietzny U., Jany K.-D.;
"Purification and characterization of two phytases from Escherichia
                                                                                                                                                                                     CHARACTERIZATION.

MEDLINE=20161462; PubMed=10696472; DOI=10.1139/cjm-46-1-59;
Golovan S., Wang G., Zhang J., Forsberg C.W.;
"Characterization and overproduction of the Escherichia coli appA encoded bifunctional enzyme that exhibits both phytase and acid
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MUTAGENESIS.
MEDLINE=93054596; PubMed=1429631;
Ostanin K., Harms E.H., Stevis P.E., Kuciel R., Zhou M.-M.,
                             MEDLINE=92049231; PubMed=1658595; DOI=10.1007/BF00267454;
Dassa J., Fsihi H., Marck C., Dion M., Kieffer-Bontemps M.,
Boquet P.L.;
                                                                                                 Greiner R., Jany K.-D.; "Characterization of a phytase from Escherichia coli."; Biol. Chem. Hoppe-Seyler 372:664-665(1991).
                                                                                           CHARACTERIZATION, AND PROTEIN SEQUENCE OF 23-34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; MS8708; AAA72086.1; -; Genomic_DNA.

EMBL; U00096; AAC74065.1; -; Genomic_DNA.

EMBL; D90735; BAA35745.1; -; Genomic_DNA.

EMBL; X05471; CAA29031.1; -; Genomic_DNA.

EMBL; X05471; CAA29031.1; -; Genomic_DNA.

EMBL; BS8708; -; NOT_ANNOTATED_CDS; Genomic_DNA.

PIR; BS67381; AABA20286.1; -; Genomic_DNA.

PIR; BS6733; AF820286.1; -; Genomic_DNA.

PIR; BS6733; AF820286.1; -; Genomic_DNA.

PIR; BS6733; AF820286.1; -; Genomic_DNA.
              NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-17.
                                                                                                                                                                        Arch. Biochem. Biophys. 303:107-113(1993).
                                                                                                                                                                                                                            phosphatase activities.";
Can. J. Microbiol. 46:59-71(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IDKL; X-ray; A/B=23-432.

1 IDKW; X-ray; A=23-432.

1 IDKW; X-ray; A=23-432.

1 IDKO; X-ray; A=23-432.

1 IDKP; X-ray; A=23-432.
Biochimie 69:215-221(1987).
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PDB;
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PDB;
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3D-structure, Complete professes, Direct protein sequencing, Hydrolase, Multifunctional enzyme; Periplasmic; Signal.

SIGNAL
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EL -> DV (in Ref. 4).
D -> S (in Ref. 4).
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PDB; 1DKQ; X-ray; A=23-432.
SWISS-2DPAGE; P07102; COLI.
GenomeReviews; U00096_GR; b0980.
GEODBASE; BEB047; -
ECOGEne; EG10049; appA.
BioCyc; ECOCyc:APPA-MONOMER; -.
InterPro; IPR001560; HisAc_phsphtse.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00779; HIS_ACID_PHOSPHAT_2; 1.
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Enterobacteriaceae; Escherichia.
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                                                                                                         Length
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
                                              6510C6C579177F11 CRC64;
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HSSP; P07102; 1DRM.
SMR; OGG088; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000566; HisAc, phosphte.
Pfam; PF0028; Acid_phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT 1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 1; 1.
                                                                                                   Score 2235; DB 2;
Pred. No. 7.6e-163;
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Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
Giang B., Hou Y., Yu J., Jin Q.;
"Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery."
Nucleic Acids Res. 33:6445-6458(2005).
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27-SEP-2006, entry version 1.
27-SEP-2006, entry version 5.
Phosphoanhydride phosphorylase.
Name=appA; OrderedLocusNames=SSO_0987; ORFNames=SSO_0987;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                             Length 432;
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                                                                                          Score 2235; DB 1;
Pred. No. 7.6e-163;
0; Mismatches 2;
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GO; GO:0003993; F:acid phosphatase actīvity; IEA.
InterPro; IPR000566; HisAc_phophtse.
Pfan; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIE_ACID PHOSPHAT 1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN_1.
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Matches 430; Conservative
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Q3Z3E1;
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QERKD7 ECOLI
QBRKD7;
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Distributed under the Creative Commons Attribution-NoDerivs License
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Enterobacteriaceae, Escherichia.
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MEDLINE=93054596; PubMed=1429631;
Ostanin K., Harms E.H., Stevis P.E., Kuciel R., Zhou M.-M., van Etten R.L.;
                                                                          2; Indels
                                      Length
5B355D76E7377737 CRC64;
                                    Score 2231; DB 2;
Pred. No. 1.5e-162;
1; Mismatches 2;
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01-JUN-2002, sequence version 1.
07-FEB-2006, entry version 13.
Periplasmic phosphoanhydride phosphohydrolase.
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J. Bacteriol. 172:5497-5500(1990)
47056 MW;
                                  Query Match 96.9%;
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pH 2.5 acid phosphatase and
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Enterobacteriaceae; Escherichia.
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MEDLINE-93054596; PubMed-1429631;
Ostanin K., Harms E.H., Stevis P.E., Kuciel R., Zhou M.-M.,
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                  432 AA; 46972 MW; AF86C41EA6193AC5 CRC64;
SMR; QBRKD6; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfan; PF00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNRNOWN_1.
                                                                                                                                                                                                                                                                Match 96.8%; Score 2229; DB 2; Local Similarity 99.3%; Pred. No. 2.2e-162; les 429; Conservative 0; Mismatches 3;
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07-FEB-2006, entry version 13.
Periplasmic phosphoanhydride phosphohydrolase
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Dassa J., Marck C., Boquet P.L.;
"The complete nucleotide sequence of
reveals significant homology between
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QBRKD8;

QBRKD8;

O1-JUN-2002, integrated into UniProtKB/TrEMBL.

O1-JUN-2002, sequence version 1.

O7-FEB-2006, entry version 13.

Periplasmic phosphoanhydride phosphohydrolase.

Periplasmic phosphoanhydride phosphohydrolase.

Name-sppA;

Escherichia coli.

C Bacteria; Proteobacteria; Gammaproteobacteria; Encenterobacteriaceae; Escherichia.
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Best Local (
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HSSP; P07102;
SMR; Q8RKD7; 2:
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SEQUENCE
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=90368616; PubMed=2168385;
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GO; GO:0003993; F:acid phosphatase activit GO; GO:0016787; F:hydrolase activity; IEA. InterPro: IPR00560; HisAc phsphtse. Pfam; PF00328; Acid phosphat A; 1.

PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.

PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNK
                               NCBI_TaxID=562;
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1DKM.
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J. Bacteriol. 172:5497-5500/**
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SEQUENCE
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HSSP; P07102; 1DKM.
SMR; OBKKDB; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_Dhsphate.
Pfam; PF00328; Acid_Dhosphat_A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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Harms E.H., Stevis P.
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"The complete nucleotide sequence of reveals significant homology between glucose-1-phosphatase.";
J. Bacteriol 170
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SMR; Q8RKE0; 23-432.
GO; GO:0003993; F: acid phosphatase activity;
GO; GO:00016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc phsphtse.
Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOW
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Escherichia coli
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cherichia coli acid phosphatase.";
Biol. Chem. 267:22830-22836(1992).
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E.H., Stevis P.B.,
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06-DEC-2005, integrated into
06-DEC-2005, sequence versio
07-FEB-2006, entry version 4
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PubMed=16275786; DOI=10.1093/nax/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., T
Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L
Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z.
Qlang B., Hou Y., Yu J., Jin Q.;
"Genome dynamics and diversity of Shigella species, the agents of bacillary dysentery.";
Nucleic Acids Res. 33:6445-6458(2005).
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SEQUENCE
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Name=appA; OrderedLocusNames-SBO 2250;
Shigella boydii serotype 4 (strain Sb227).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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GO; GO:0003993;
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GO; GO:0016787; F:hydrolase activity; IEA.
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Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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J. Bacteriol. 172:5497-5500(1990).
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MEDLINE=90368616; PubMed=2168385;
Dassa J., Marck C., Boquet P.L.;

"The complete nucleotide sequence of the reveals significant homology between piglucose-1-phosphatase.";
J. Bacteriol. 172:5497-5500(1990).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003993; F:acid phosphatase actions (Go; GO:0016787; F:hydrolase activity; InterPro; IPR000560; HisAc_phsphtee. pfam; PF00328; Acid_phosphat A; 1. PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; PS00616; HIS_ACID_PHOSPHAT_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Overexpression, site-directed mutagenesis, Escherichia coli acid phosphatase."; J. Biol. Chem. 267:22830-22836(1992).
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MEDLINE=93054596; PubMed=1429631;
MEDLINE=94054596; PubMed=1429631;
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HSSP; P07102; LDKM.
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AC Q83RW2;
DT 01-JUN-2005, s
DT 05-JUL-2005, s
DT 05-JUL-2005, s
DT 05-JUL-2005, s
DT 07-PEB-2006, e
DE Phosphoanhydrid
GN Name-appA, Ord
OS Shigella flexn
OC Enterobacteria
OX NCBI TaxID=623
RN NUCLEOTIDE SEQ
RC STRAIN=301 / S
RX MEDLINE=227724
RA Jin Q., Yuan
RA Yang J., Yang
RA Yang J., Yang
RA Cheng H., Yang
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RA Yu J.;
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SEQUENCE 432 AA; 47106 MW; 25093A5392B9C18C C1
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                                                                                                                                                                                                                                                                                                           TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
     EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
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EMBL; AY496073; AAR87658.1; -; Genomic_DNA.

SMR; Q6KK08; 23-432.

G0; G0:0003993; F:acid phosphatase activity; IEA.

InterPro; IPR000560; HisAc_phsphtse.

Pfam; PF00328; Acid_phosphat_A; 1.

PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.

PROSITE; PS00778; HIS ACID_PHOSPHAT 2; UNKNOWN 1.

CHAIN

CHAIN

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432

A7042 MW; 71B0E5EED2EA2674 CRC64;
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MEDLINE=99194564; PubMed=10092520; DOI=10.1006/bbrc.1999.0361;
Rodriguez E., Han Y., Lei X.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALFSELKVSADNVSLTGAVSLASMLT
                                                                                                                                                                           TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQPGQVAIIADVDERTRKTGE
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                                                                       AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
                                                                                                                                                                                                                                                                               MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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Pred. No. 9.1e-162;
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RESULT 13
Q7UDO8_SHIFL PRELIMINARY; PRT; 432 AA.
AC Q7UDO8;
D7 01-CCT-2003, integrated into UniprotKE/TrEMBL.
D7 01-CCT-2003, sequence version 1.
D7 01-CCT-2003, sequence version 1.
D7 07-MAR-2006, entry version 1.
D7 07-MAR-2006, entry version 1.
D8 Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase.
D8 Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase.
D8 Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase.
D9 Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase.
D1 07-MAR-2006, entry version 1.
D7 07-MAR-2006, entry version 1.
D8 Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase.
D8 Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase.
D8 Name-apph, OrderedLocusNames=S1048; ORFNames=S_1048;
D8 Shigella flexneri.
D8 STRAIN=2457T / ATCC 70930 / Serotype 2a;
D8 MICLEDTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
D8 NCBI_TaxID=623;
D8 NCBI_TaxID=623;
D8 NCBI_TaxID=623;
D8 NCBI_TaxID=623;
D8 NCCBI_TaxID=623;
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STRAIN=24577 / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; pubmed=12704152;

DOI=10.1128/IAI.71.5.2775-2786.2003;

Wei J., Goldborg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 24577.";

Infect. Immun. 71:2775-2786(2003).
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Enterobacteriaceae; Shigella.
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AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
                                                                                                                                                   TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
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QSCW75 ECOL6
ID QSCW75;
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AC QSCW75;
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Pfam; PF00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1;
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2;
Complete proteome.
SEQUENCE 446 AA; 48606 MW; F1308CD6
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HSSP; P07102; 1DKQ.
SMR; Q8CW75; 33-442.
BioCyc; ECOL199310:C1121-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRALM=06:H1 / CFT073 / ATCC 700928 / UPEC;
MEDLINE=22388234; PubMed=12471157; DDI=10:1073/pnas:252529799;
MEDLINE=22388234; PubMed=12471157; DDI=10:1073/pnas:252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0003993; F:acid phosphatase activity;
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                             TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
                                                                                                       MKAILIPFLSLLIPLTPKSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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                                                                                                                                                                                                                 Score 2213; DB 2;
Pred. No. 3.9e-161;
3; Mismatches 4;
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8 밁 Ś 밁

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RESULT 15
Q7AFW3 ECO57
ID Q7AFW3;
AC Q7AFW3;
DT 05-JUL-2004, s
DT 05-JUL-2004, s
DT 05-JUL-2004, s
DT 07-FEB-2006, e
DE Phosphoanhydrid
GN OrderedLocusNa
OS Bacteria; Prot
CC Enterobacteria
OX NCBI TaxID=833
RN NULLEOTIDE SEQ
RC STRAIN=0157;H7
RX MEDLINE=211562
RA HANC.-G., Obt
RA HANGLING=211562
RA HANG.-G., Obt
RA HANG.-G., Obt
RA C.-G., Obt
RA C.-
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Best Local S
Matches 427
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STRAIN=0157:H7 / Sakai / RIMD 0509952 / BEG.

MEDLINE=21156231, PubMed=11258796; DOI=10.1023/dnares/8.1.11;

MEDLINE=21156231, PubMed=11258796; DOI=10.1023/dnares/8.1.11;

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakkawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT 1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.
SEQUENCE 434 AA; 47337 MW; P197DF7D1869F9C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BA000007; BAB34559.1; -; Genomic_DNA. SMR; Q7AFW3; 25-434. GO; GO:0003993; F:acid_phosphatase_activity;
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 10.
Phosphoanhydride phosphorylase.
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WPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKT
                                                                                                                                          MKAILIPFLSLLIPLTPQSAFAQS--EPELKLESVVIVSRHGVRAPTKATQLMQDVTPDA 58
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                                                     RWRRLSDNSQWIQVSLVFQTLQQMRDKTFLSLNTFPGEVKLTLAGCEERNAQGMCSLAGF
                                                                                   AALTEHPPQKQAYGVTLFTSVLFIAGHDTNLANLGGALELNWTLFGQPDNTPPGGELVFE
                                                                                                                            LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM
                                                                                                                                                                                                                 GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT
            TQIVNEARIPACSL
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TOIVNEARIPACSL
                                         RWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGF
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Search co Job time completed: June 13, me : 196.752 secs 2006, 10:28:32

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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A_Geneseq_8:*
1: geneseqp1980s:*
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Copyright (c) 1993 - 2006
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o	U	4.	· w	N	–	No.	Regult
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ALIGNMENTS

Escherichia coli Kl2 appA phytase mutant 819PH59.

29-JUL-2004 ADO50300;

(first entry)

ADO50300 standard; protein; 432

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13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                           /note= "Wild-type Misc-difference 226
                                                                                                                           /note= "Wild-type Asn replaced with Cys" Misc-difference 2,77
                                                                                                                                                                                   /note= "Wild-type Lys replaced with Cys" Misc-difference 168
                                                                                                                                                                                                     /note= "Wild-type Ala replaced with Pro" Misc-difference 97
                                                                 20-JUN-2003; 2003US-00601319.
                                                                                    13-MAY-2004.
                                                                                                     US2004091968-A1
                                                                                                                                                                   Misc-difference 181
                                                                                                                                                                                                                          Misc-difference 95
                                                                                                                                                                                                                                            Misc-difference 84
                                                                                                                                                                                                                                                     Misc-difference 68
                                                                                                                                                                                                                                                                                          Escherichia coli; K12.
Synthetic.
                                                                                                                                                                                                                                                                                                                   AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; enzyme; mutant; mutein.
97US-00910798.

99US-00259214.

99US-00291931.

99US-00318528.

2000US-00580515.

2001US-00866379.
                                                                                                                                                                          /note= "Wild-type Ser replaced with Glu"
                                                                                                                        'note=
                                                                                                                                                                                                                                note= "Wild-type Gln replaced with Trp"
                                                                                                                                                                                                                                                   note= "Wild-type Trp replaced with Glu"
                                                                                                                     "Wild-type Tyr replaced with Asp'
                                                                                                                                                          Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as guppy, zebrafish, molly, swordtail, CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase enzyme mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Mather EJ;
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(KRET/)
(GRAY/)
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GARRETT J B.
O'DONOGHUE E.
MATHER E J.
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                                               RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                     LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                                                                                                                                       AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
                                                                                                                                                                                                                                                                                                                                                   TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
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                                                                                                                                               EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
                                                                                                                                                                  EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
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                                                                                                                                                                                                                                                                                                                             TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
                                                                                                                                                                                                                                                                                                                                                                                       MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
IVNEARIPACSL 432
                           RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                      LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                                                        YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    providing nucleic acid derived from bacteria phytase activity, and expressing nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2258; DB 8;
Pred. No. 3.2e-219;
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WPI; 2005-733851/75.
N-PSDB; AED50817, AED50824.
                                                             (SHOR/)
(KRET/)
(GRAY/)
(BART/)
                                                                                                       25-MAY-2000;
24-MAY-2001;
                                                                                                                    13-APR-1999;
25-MAY-1999;
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EC 3.1.2.8; 3-phytase; recombinant protein;
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                     Mathur
                            Short
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(ODON/)
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                с JM,
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                                       SHORT J M.
KRETZ K.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
MATHUR E J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein;
                           Kretz K,
                                                                                                                                                                                                                                                                                                                                                                                                                             coli phytase mutant protein
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2000US-00580515.
2001US-00866379.
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99US-00259214.
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357
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Best Local S
Matches 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also useful in gene therapy and in production of transgenic animals. The present sequence is a Escherichia coli phytase mutant protein which is encoded by appA gene.
 Escherichia Synthetic.
                                                       enzyme; mutein; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture; osteoporosis
                                                                                                                                                       AEE75421;
                                                                                                                                                                                 AEE75421
                                          osteopathic;
                                                                                                                           23-FEB-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated or recombinant nucleic acid encoding as foodstuff, and for oil degumming, producing an a phytase enzyme supplement to an animal.
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                                                                                                                                                                                                                                                                                                                         RRLSDNSQWIQVSLVFQTLQQMRDKTFLSLNTFPGEVKLTLAGCEERNAQGMCSLAGFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
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                                                                                                                                                                                                                                                                      IVNEARIPACSL 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
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                                                                                                                                                                                                                                                                                                          RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                        EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
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                                                                                                                                                                                                                                                                                                                                                                LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                              modified appA phytase
                coli K12
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                                          food;
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                                          appA
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Pred. No. 3.2e-219;
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                                                     osteoporosis;
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The present sequence is that a novel modified phytase derived from the CR Sscherichia coli appA protein, with improved thermal tolerance and CR protease stability compared to the wild-type. The present invention CR relates to a novel formulation, comprising at least one polypeptide CR having phytase activity, where the polypeptide is a modified sequence CR (AEE7541) derived from the Escherichia coli K-12 appA phytase CR (AEE75419). The modification of the enzyme, comprising a series of CR (AEE75419). The modification of the enzyme, comprising a series of CR (AEE75419). The modification also claims a pharmaceutical composition; a CR kit; an immobilized phytase; a fertilizer or soil additive, a liquid CR supplement for preventing muscle cramps; a hydrating agent; a tissue CR culture or cell culture media; and a plant food additive, all comprising CR the novel phytase, and a method of reducing pollution and increasing CR culture tavailability in an environment or environmental sample by CR degrading environmental phytic acid. The novel enzyme is a dietary culture media; and preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 10; 82pp; English.
                                                                                                                                                                                                                                                                                                                                  Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baum
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(KRET/)
(GRAY/)
(BART/)
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DB; AEE75420.
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOCHUE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAUM W.
ROBERTSON D
ZORNER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robertson
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99US-00259214.

99US-00251931.

99US-00318528.

2000US-00580515.

2001US-00866379.
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277
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Zorner
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01-MAR-1999;
13-APR-1999;
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                                                                                                     24-MAY-2002;
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                                                                                                                                                                                                          The invention discloses a new isolated or recombinant nucleic acid which ce encodes a polypeptide having a phytase activity. Also claimed is a composite of the nucleic acid, a vector comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, a phytase message in a cell, a heterodimer comprising the translation of casecond domain, an array comprising immobilised polypeptide or nucleic acid, a hybridoma comprising a mantibody that specifically binds to the card, a hybridoma comprising a nantibody that specifically binds to the card, a hybridoma comprising a manimal, an edible enzyme delivery card, a feed composition, a soybean meal, isolating or identifying the polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, making an anti-phytase antibody, producing a recombinant polypeptide, determining whether a compound binds to the polypeptide, continuity and the entranslative films analysis, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a digestive system and processing of corn and sorghum kernels. The phytase cativity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or case an aid in phytate digestion. The sequence presented is the modified
                                                                                                                                       Matches 432;
                                                                                                                                                      Query Match
Best Local
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Mathur EJ;
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25-MAY-2000;
24-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w nucleic acid encoding a polypeptide having improving the feeding value of phytate rich phytate digestion.
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Pred. No. 3.3e-219;
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             K12 appA phytase. The enzyme has phytase activity and improved thermal tolerance when compared with wild-type phytase. It has improved protease stability at low pH. The recombinant phytase is useful for improving the nutritional value of phytate-containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in treatment processes and for in the consument of the systems.
                                                                                                                                                                                                                            New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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                                                                                                                                               patent discloses recombinant bacterial phytase from Escherichia coli
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Misc-difference

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"Wild-type Gln substituted

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Condification from W68E, 084W, A95P, K97C, S168E, R180Y, N226C or Y277D.
CC Also included the E. coli apph gene ADA194450 and having amino acids correctly derived from it) or its mutant sequence ADA19455.
CC derived from it) or its mutant sequence ADA19450 are phytate-containing foodstuff by contacting the phytate-containing foodstuff by contacting the phytate-containing foodstuff by contacting the phytate-containing foodstuff), a method to produce an animal feed containing a containing foodstuff), a method to produce an animal feed containing a converting the plant cells, plant part or plant under conditions where the nucleotide sequence is expressed and converting the plant cells, plants or plants or plant into a composition for animal feed composition for animals (comprising the plant seeds, plant cells, plant parts or plants in admixture with a phytate-containing codstuff), a method to treat a human or an animal able to benefit from diseative enhancement by the activity of an exogenous phytate enzymes comprising administering to the human or animal the plant seeds, plant cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence encoding a phytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a polypeptide having phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The containing the plant entry of an expression of animal feed and for enhancing digestion in humans and animals. The present containing the presents E. coli K12 mutant phytase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 59; Fig 8; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing
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(KRET/)
(GRAY/)
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25-MAY-1999;
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01-MAR-1999;
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(GARR/)
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) BARTON N R.
) GARRETT J B.
) O' DONOGHUE E.
) MATHUR E J.
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99US-00318528.
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Best Local Similarity
Matches 430; Conser
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                                                                                                                              02-NOV-2000
                                                                                                                                                                                                               environmental pollution; pig.
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20-FEB-2001
                                                                                                                                                                                                                                                                                                                        AAB36257
            N-PSDB; AAC68294
                     WPI; 2000-687245/67
                                         Forsberg
                                                                                   23-APR-1999;
                                                                                                       20-APR-2000; 2000WO-CA000430
                                                                                                                                                  WO200064247-A1
                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                          Transgenic animal; salivary protein; phytase; phosphorus; animal growth;
                                                                                                                                                                                                                                               Lama2/APPA plasmid translated sequence
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                                                                                                                                                                                                                                                                                                                         standard; protein; 432
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                                                                GUELPH
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(first entry)
                                           Golovan
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1. No. 3.5e-216;
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Best Local Similarity
Matches 424; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides transgenic animals which produce desired proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet being excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the E. coil APPA phytase coding sequence. (Updated on 12-SEP-2003 to standardise OS field)
                                  Rattus sp.
Escherichia
                                                                   environmental
                                                                              Transgenic
                                                                                                   R15/APPA plasmid translated sequence
                                                                                                                                                            AAB36261;
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                                                                            animal; salivary protein; phytase; phosphorus;
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98.1%;
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Pred. No. 1.6e
0; Mismatches
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No. 1.6e-211;
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WO200064247-A1

RESULT 9
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AAB36262

standard; protein; 432

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nucleic sequence including a heterologous transgene construct encoding the
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N-PSDB; AAC68298.
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                        IVNEARIPACSL
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98.1%;
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Pred. No. 1.6e-211;
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Best Local Similarity
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                                  LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     The present invention provides transgenic animals which produce desired proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet being excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the E. coli APPA phytase coding sequence. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nucleic sequence including a heterologous transgene construct encoding the
                                                                                                                                                                                                                                                                                                        Sequence 432 AA;
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                                             The present invention provides transgenic animals which produce desired proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phyrate in the dilet being excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the B. coil APPA phytase coding sequence. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                            Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nuclei sequence including a heterologous transgene construct encoding
  Sequence
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ARBSULT 12
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AXX AAB36
AX AAB36
DT 12-SE
DT 20-FE
XX Trans
KW Trans
KW envir
XXX Esche
OS Esche
OS Chime
XX WO200
XX 02-N0
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Best Local S
Matches 424
Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nucleisequence including a heterologous transgene construct encoding
                                                                                                                                                                                                                                                                                                                                                                                               AAB36263
                                                                                  Forsberg
                                                                                                                                                        20-APR-2000;
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                                                                                                                                                                                                                               Chimeric.
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20-FEB-2001
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                                                 2000-687245/67.
DB; AAC68300.
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                                                                                                                                                                                                                                                                                                                                                                                              standard; protein;
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                                                                                                                                                                                                                                                                                      animal; salivary protein;
                                                                                                                                                                                                                                                                                                             plasmid translated sequence.
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                                                                                                           GUELPH
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(first entry)
                                                                                    Golovan
                                                                                                                                                                                                                                                                           pollution;
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Pred. No. 1.6e-21
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ARBS6260
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DT 112-SE
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XX Trans
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OS Rattu
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XX WO200
PD 02-NC
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Best Local S
Matches 424
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                                                                                                       Transgenic animal; salivary protein; phytase; phosphorus; environmental pollution; pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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               02-NOV-2000
                                                                       Rattus sp.
Escherichia
                                                                                                                                              R15/APPA plasmid translated
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20-FEB-2001
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al Similarity 98.1%;
424; Conservative
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                                                                                                                                                                                                                                 standard;
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Pred. No. 1.6e-211;
0; Mismatches 8;
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AAU77775 sta AAU77775; 05-JUN-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides transgenic animals which produce desired proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet being excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the E. coli APPA phytase coding sequence. (Updatec on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nucleic acid sequence including a heterologous transgene construct encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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IVNEARIPACSL
                                            RRLSDNSQWIQVSLVFQTLQQMRDKTFLSLNTFPGEVKLTLAGCEERNAQGMCSLAGFTQ
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milarity 98.1%;
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Pred. No. 1.6e-211;
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                   AAE15807 standard; protein, 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 10pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel phytase gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to a novel phytase gene, a recombinant phytase gene their uses. This is the amino acid sequence of the phytase associated
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                                                                                                                                                                                                                                                                                    AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
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No. 1.6e-211;
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Matches 424
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bacterial phytase for e.g. improving the nutritional value of phytate containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 54; Fig 8; 170pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; nutritional value; feed treatment process; therap thermal tolerance; growth performance; alcoholic drink; biopulping; non-alcoholic drink; biobleaching.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD25463.
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                           YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
                                                                                     AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
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Qy 241 EIFILQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA 300 Db 241 EIFILQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA 300 Qy 301 LTPHPPQKQAYGVTLPTSVLFTAGHDTNLANLGGALELWMTLPGQPDNTPPGGELVPERW 360 Db 301 LTPHPPQKQAYGVTLPTSVLFTAGHDTNLANLGGALELWMTLPGQPDNTPPGGELVPERW 360 Qy 361 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPGGEVKLTLAGCEERNAQGMCSLAGFTQ 420 Qy 361 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420	Search Job ti	ф	Ş	망	Ş	Вb	γ	뫄	δ
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IBBUED PATENTS AA:*

| / EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
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| EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
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| EMC Celerra SIDS3/ptodata/2/iaa/BCTUS COMB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-866-379-2
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US-09-866-041x-1
US-09-489-039A-7512
US-09-489-039A-13501
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US-09-684-855-106
US-09-684-855-128
US-09-684-855-151
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         Sequence 10, Appl
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 128, Appli
Sequence 128, Appli
Sequence 128, Appli
Sequence 128, Appli
Sequence 129, Appli
Sequence 120, Appli
Sequence 121, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 33, Appli
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	61 TWPVKLGELTPRGGELI 61 TWPVKLGELTPRGGELI	2y 1 MKAILIPPLSILIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60 	Query Match 98.7%; Score 2228; DB 2; Length 430; Best Local Similarity 99.5%; Pred. No. 2.3e-227; Matches 430; Conservative 0; Mismatches 0; Indels 2; Gaps 2;	US-09-866-379-10 Sequence 10, Application US/09866379 Patent No. 685365 GENERAL INFORMATION: APPLICANT: SHORT, Jay APPLICANT: SHORT, Jay APPLICANT: GARRETT, Keith APPLICANT: GARRETT, James APPLICANT: GARRETT, James APPLICANT: O'DONOGHUE, Eileen TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF FILE REFERBAGE: DUER1370-7 CURRENT APPLICATION NUMBER: US/09/866,379 CURRENT APPLICATION NUMBER: US/09/866,379 CURRENT FILING DATE: 2000-05-24 PRIOR APPLICATION NUMBER: US 09/318,528 PRIOR APPLICATION NUMBER: US 09/318,528 PRIOR APPLICATION NUMBER: US 09/318,528 PRIOR APPLICATION NUMBER: US 09/291,931 PRIOR APPLICATION NUMBER: US 09/259,214 PRIOR APPLICATION NUMBER:	ALIGNMENTS	27 126 5.6 465 2 US-09-273-871A-8 Sequence 8, Appli 28 126 5.6 465 2 US-10-083-452-8 Sequence 8, Appli 29 126 5.6 465 2 US-09-635-504-33 Sequence 73, Appl 31 126 5.6 465 3 US-10-262-848-78 Sequence 78, Appl 31 126 5.5 440 2 US-09-684-855-129 Sequence 107, Appl 32 125 5.5 440 2 US-09-684-855-129 Sequence 129, Appl 34 125 5.5 440 2 US-09-684-855-129 Sequence 129, Appl 35 125 5.5 440 2 US-09-684-855-129 Sequence 152, Appl 36 124 5.5 467 2 US-09-684-855-165 Sequence 165, Appl 37 124 5.5 467 2 US-09-684-855-165 Sequence 130, Appl 38 118 5.2 440 2 US-09-684-855-130 Sequence 130, Appl 39 118 5.2 440 2 US-09-684-855-130 Sequence 130, Appl 41 118 5.2 440 2 US-09-684-855-130 Sequence 130, Appl 42 118 5.2 440 2 US-09-684-855-130 Sequence 153, Appl 43 118 5.2 440 2 US-09-684-855-130 Sequence 153, Appl 44 1 118 5.2 465 2 US-09-448-718-80 Sequence 80, Appl 45 117 5.2 465 2 US-10-062-848-79 Sequence 80, Appl 45 117 5.2 465 2 US-10-062-848-79 Sequence 79, Appl 45 117 5.2 465 2 US-10-062-848-79 Sequence 79, Appl

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121 AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH 180

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; NUMBER OF SEQ ID NOS: 10
; SOFTMARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-866-379-8
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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Matches
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APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
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            AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
                                                  TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
                                                                 TWPVKLGELTPRGGELTAYLGHYWRQRLVADGLLPKCGCPQSGQVATTADVDERTRKTGE
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AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
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98.1%;
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Best Local Similarity
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; TYPE: PRT; ORGANISM: Escherichia US-09-715-477-1
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CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 199-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-D)
FILE REFERENCE: 19603/4031
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                       RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLWTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420
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                                                                                                             LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
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RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 6.1e-222;
0; Mismatches 9;
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APPLICANT: Kretz, Keith
FILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVERL370.1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                             RESULT 5
US-09-318-528-2
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US-09-259-214-2
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GENERAL INFORMATION:
APPLICANT: K-etz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
                                                                                 Sequence 2, Application Patent No. 6183740
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Best Local Similarity
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ORGANISM: Escherichia
-09-259-214-2
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Pred. No. 2.7e-221;
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; TYPE: PRT ; ORGANISM: Escherichia US-09-291-931-2

SEQ ID NO 2

LENGTH:

440

NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows

Version

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GENERAL INFORMATION:

APPLICANT: Kretz, Keith
ITITLE OF INVENTION: NOVEL PHYTASE
ITITLE OF INVENTION: NOVEL PHYTASE
CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
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; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: 08/910,798
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
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Best Local Similarity
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ORGANISM: Escherichia
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Pred. No. 2.7e-221;
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Sequence 2, Application US/09580515
Patent No. 6720014
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/580,515
CURRENT FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/2921,931
PRIOR APPLICATION NUMBER: 09/2921,931
PRIOR APPLICATION NUMBER: 09/293,798
PRIOR APPLICATION NUMBER: 09/293,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
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US-09-580-515-2
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Best Local Similarity
Matches 422; Conserv
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Pred. No. 2.7e-221;
0; Mismatches 10; Indels
                                                                                                                                      Score 2171; DB 2;
Pred. No. 2.7e-221;
0; Mismatches 10;
                                                                                                                                                                             Length 440;
                                                                                                                                        Indels
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APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
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; TYPE: PRT
; ORGANISM: Escherichia
US-09-866-379-2
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US-09-866-379-2
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Nelson
APPLICANT: GARRETT, James
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Best Local Similarity
Matches 422; Conserv
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Pred. No. 2.7e-221;
0; Mismatches 10;
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THEREOF

420

360

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Gaps

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Sequence 3, Application US/09715477
PALENT NO. 6841370
GENERAL INFORMATION:
APPLICANT: Le1, Xingen
ITTLE OF INVENTION: SITE-DIRECTED MUTAGENES
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR PILING DATE: 1999-11-18
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SEQ ID NO 3
LENGTH: 432
TYPE: PRT
GRGANISM: Escherichia coli
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Best Local Similarity
Matches 420; Conserv
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                                                           EIFLLQQAQGMPBPGWGRITDSHQWNTLLSLHNAQFDLLQRTPBVARSRATPLLDLIKTA
                                                                                              ROTAFRELERVLNFPQSNLNLKREKQNESCNLTQALPSELKVSADNVSLTGAVSLASMLT
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Pred. No. 8e-220;
2; Mismatches 10;
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APPLICANT: Lei, Xingen
TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVED PHY
FILE REFERENCES: 19603/2798
CURRENT APPLICATION NUMBER: US/10/266,041A
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
PRIOR STILING DATE: 2000-03-31
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US-10-266-041A-1
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Best Local Similarity
Matches 418; Conserve
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TYPE: PRT
ORGANISM: Escherichia
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                 IVNEARIPACSL 432
                                                                                 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                                                                                                                                  EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
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                                                              RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 9.3e-219;
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RESULT 11
US-09-540-149A-1
; Sequence 1, Application US/09540149A
; Patent No. 6511699
; GENERAL INFORMATION:

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ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (433)
; OTHER INFORMATION: Xaa at position 433 in this sequence is unknown US-09-540-149A-1
                                                                                                                                                                                                                                                                     RESULT 12
US-08-910-798-2
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TITLE OF INVENTION: SZZYMES WITH IMPROVED PHYTASE .
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
                                                                                                                                                                                                              Sequence 2, Application Patent No. 5876997 GENERAL INFORMATION:
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Best Local (
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COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                           TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   APPLICANT: KRETZ
                                                                 STREET: 4225 Execu
CITY: La Jolla
STATE: California
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Local Similarity 96.8%;
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Pred. No. 9.3e-219;
0; Mismatches 14;
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US-09-489-039A-7512
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                                                                                                                                                            Patent No. 6610836
GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 7512, App
Patent No. 6610836
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           APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/9/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQ ID NOS:
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NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear

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93.8%;
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Pred. No. 6.5e-210;
0; Mismatches 10;
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RESULT 14
US-09-489-039A-13501
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7512
                                                                                                                                                                                                                                                                                             Query Match 16.9
Best Local Similarity 26.3
Matches 117, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13501
LENGTH: 522
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING.
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER: OF SEQ ID NOS: 14342
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cal Similarity 32.6%; Pred. No. 1.5e-48;
136; Conservative 70; Mismatches 181; Indels
                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 WIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEA 425
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                                                                                   164 TEWTTHDGELTGHGYAAVVNKGRAEGOHYROLGLL-OAGCPTAESIYVRASPLORTRATA
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                                                                                                                                                                                                                                        2 KAILIPPLSLLIPLTP-QSAFAQSEPELKLESVVIVSRHGVRAPTKAT-QLMQDVTPDAW
EAFAAGLAFDCAITVHTQADTSSFDFLFNFLKTGVCQLDNANVTDAILERAGGSIADFTG
                                                                                                                                                                                        GULREFIACALPULALQSAAA---ADWQLEKVVELSRHGIRPPTAGNREAIBAATGRPW
                                                                                                                                   PTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMKIEYVYQSTEQLRNADALTLQAPPQRVTLALNGCPV-DDQGPCPLETFKMVINEA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKDQVAWGETASDKQWRVLSKLKNGYQDSLFTSVAVAQNVAKPLVKYIDNALVGEGASK- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P--EPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATFLLDLIKTALTPHPPQKQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDYRNSPSC----KEKKVCSLSEGKDTFSAGYQQEPGVSGPLKVGNSLVDAFTLQYYEGF 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVHHQPQMGTMDPTFNPVITDDSPAFREKALQAMEKERQGMQLTE-----SYKLLETM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AKVTLLVGHDSNIASLLTALDFKPYQLÞGQYERTÞIGGKLLFQRWHDSAGNRD 363
                                                                                                                                                                                                                                                                                                16.9%; Score 381; DB 2; Length 522, 26.3%; Pred. No. 3.3e-31; ative 73; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 421;
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APPLICANT: PASAMONTES, Luis
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: Van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
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SOFTWARE: PatentIn Ver.
SEQ ID NO 3
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APPLICANT: KOSTREW
APPLICANT: PASAMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09044718 Patent No. 6391605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 HYQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASML
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                                                       -- LPGVTLTDEDVVSLMDMCSFDTV----
                                                                                                       QALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL--
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     HN--AQFDLLQR-
                                                                                                                                                               CTKFEASQLGDEV-----AANFTALFAPDIR-----ARAEKH-----
                                                                                                                                                                                                                 C-QLDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCSLT
                                                                                                                                                                                                                                                                                                                   ADVDERTRKTGEAFAAGL------APDCAITVHTQADTSSPDPLFNPLKTGV 154
                                                                                                                                                                                                                                                                                                                                                                           KGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVP-----FIR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                -----WPTWPVKLG--ELTPRGGELIAYLG--HYWRQRLVADGLLPKCGCPQSGQVAII 108
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TPE-VARSRATPLLDLIKT--ALTPHP 305
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Perfect score:
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        seq length: 0
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Match
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1: /EMC Celerra SIDS3/ptodata/1/pubpaa/US09 NEW PUB.pep:*

2: /EMC_Celerra SIDS3/ptodata/1/pubpaa/US06_NEW PUB.pep:*

3: /EMC_Celerra SIDS3/ptodata/1/pubpaa/US07_NEW PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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US-10-527-411-58
US-10-527-411-59
US-10-527-411-44
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Biocceleration Ltd.
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RESULT 1 US-10-511-937-2424 ; Sequence 2424, Application US/10511937		-	44	43				39	38	37	36	35	34	ω ω	32	31	30	29				
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)51193 <i>7</i>	ALIGNMENTS	US-10-953-349-33870	US-10-953-349-33871	US-10-471-571A-4496	-10-505-928-50	Ļ	US-11-293-697-3258	US-10-505-928-284	US-11-270-040-6	US-10-505-928-300	US-10-953-349-11733	US-10-953-349-11734	US-10-953-349-32469	US-10-953-349-32470	US-10-953-349-32471	US-10-953-349-34902	US-10-953-349-34903	US-10-953-349-34904	US-10-953-349-11735	US-11-183-325-56	US-10-527-411-46	
			33871,	4496	50.		3258		Sequence 6, Appli		11733,	11734,		32470,	32471,	34902,	æ	34904,	1173	ເກ	Sequence 46, Appl	

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APPLICANT: FIGURE (PARTICLE)

APPLICANT: ROSENBERG, Steven

ITITE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

ITITE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

ITITE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

PILE REFERENCE: 50661200104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: POT/US2003/012946

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR PILING DATE: 2002-12-20

NUMBER OF ESQ ID NOS: 3117

SOPTWARE: Patentin version 3.2

SEQ ID NO 2424

LENGTH: 635
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Best Local Similarity 20.4%;
Matches 115; Conservative 60
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GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS,
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
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APPLICANT:
APPLICANT:
APPLICANT:
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    243
                                                                                            183 TVIQLIATETCCPALQRPHSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGSCL
                                                                                                                                                                                          123 RVLFVDSVGLPAPPSIIKÄMGGŠQPGĖLQISWEĖPAPEIŠDFLRYELRYGPRDPKNSTGP 182
                                               77 IAYL---GHYWRQ-RLVADGLLPKCGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAI 132
                                                                                                                                 2 KAILIPFLSLLIPLTPQSAFAQSEP-ELKL---ESVVIVS-----RHGVRAPTKAT--
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Woodward, Robert
Ly, Ngoc
Prentice, James
ISGLOPGNSYWLOLKSEPDG-ISLGGSWGSWSLPVTVDL-----PGDAVALGL-----
                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                                            Score 101.5; DB 6; Length 635; Pred. No. 0.23; Mismatches 195; Indels 193;
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US-11-293-697-2758
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2758, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                              ALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGW 256
                                                                                                                                                                                                     VWLLSRAEVRPRSALGSSRRGLGDKGPRSRRAAEFTQARPTRKRRTPGGGRPEAGC----
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                                                                                                   ----VTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCSLTQ 214
                                                                                                                                     ---WLENRRQRRRKAG-AERAGAGP----TLTPPLPAGSPDPP-SPAATAAPQPEQRPHL
                                                                                                                                                                                                                                                                          LLPELPTQISSSRPTRPRRCKSSSRPHL------ARGRRSPLKAAQ--QDRGLPAWG
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 -SGSGAAMTGSWA--
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Pred. No. 0.18;
Pred. No. 0.18;
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 ---APPRPAW 274
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APPLICANT: Numez, Gabriel
APPLICANT: Numez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular:
FILE REFERENCE: UM-06967
CURRENT FILING UM-06967: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOPTWARE: Patentin version 3.1
LENGTH: 765
TWORD: DOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Sequence 34, Application US/11317329
Publication No. US20060105413A1
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TITLE OP INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VTLPT----SVLFIAGHDTNL------ANLGGALELNWT
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21.6%;
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%; Pred. No. 1.6;
46; Mismatches 144;
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US-11-317-329-35
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                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Homo sapiens US-11-317-329-35
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SEQ ID NO 35
LENGTH: 765
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                                                                                                                                                                                                                                    Query Match 4.1%; Score 93.5; DB 7; Length 765; Best Local Similarity 21.6%; Pred. No. 1.6; Matches 88; Conservative 46; Mismatches 144; Indels 129;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
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                                   113 ERTRKTGEAFAAGLAP-------DCAITVHTQADTSSPD-----PLFNPLKTGVCQ 156
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US-11-317-329-36
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
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APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
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TYPE: PRT
ORGANISM: Homo
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                                        ----VTLPT----SVLFIAGHDTNL-----ANLGGALELNWT 341
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YGASLELPTHQGWTPLHLAAYKGHLEIIHLLAESHANMGALGAVNWT
                                                                                                                          HNAQFDLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYG---------
                                                                                                                                                                     -----AEGKTPLHVAAYFGHVSLVKLLT------SQGAELDAQQRNLRTPL
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                                                                                  VERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYLICKMLLR 581
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RESULT 7 US-11-317-329-37

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; TYPE: PRT ; ORGANISM: Homo sapiens US-11-317-329-38
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US-11-317-329-38
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US-11-317-329-37
                                                                                                                                                                                                                                                                                                          Sequence 38, Applicate Publication No. US200 GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
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Best Local (
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                                                                                SEQ ID NO 38
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Publication No. US20060105413A1
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APPLICANT: Inohara, Machiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
                                                                                                                                                                                                                            APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions
FILE REFERENCE: UM-06967
                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                           NUMBER OF SEQ ID NOS: 44
                                                                                                                                            PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
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l Similarity 21.6%;
88; Conservative '
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; Pred. No. 1.6; 
46; Mismatches 144; Indels 12
                                                                                                                                                                                                                                                  for Regulating Cellular Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ANLGGALELNWT 341
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US-11-317-329-39
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                         Local Similarity
443
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                                                                                                                                                           338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVE-----QVRLLLAHEVDVD
                                                                                                                                                                                                   61 TWPVKLGE---LTPRGGELIAYLGHYW-RQRLVADGLLPKCGCPQSGQVAII----ADVD 112
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TARLLLDHGACVDA-QEREGWTPLHLAA--QNNFENVARLLVSRQADPNLRE---
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                                                                                                                  ERTRKTGEAFAAGLAP------DCAITVHTQADTSSPD-----PLFNPLKTGVCQ 156
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                                     ----LDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCS 211
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                                                                                                                                                                                                                                                                                                                     ; Score 93.5; DB 7;
; Pred. No. 1.6;
46; Mismatches 144;
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6; Mismatches 144;
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Pred. No. 1.
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; ORGANISM: Homo sapiens
US-11-317-329-40
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Sequence 41, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
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SEQ ID NO 40
LENGTH: 765
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Best Local Similarity
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
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TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
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                                                                                                                                                                                                                                                            -----SQGABLDAQQRNLRTPL
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21.6%; Pred. No. 1.6;
htive 46; Mismatches 144;
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RESULT 12
US-11-317-329-42
j Sequence 42, Application US/11317329
publication No. US20060105413A1
GENERAL INFORMATION:
                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
US-11-317-329-42
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Query Match 4.1%; Score 93.5; Di
Best Local Similarity 21.6%; Pred. No. 1.6;
Matches 88; Conservative 46; Mismatches
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
SEQ ID NO 41
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APPLICANT: Inohara, Naohiro
TITLE OP INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR PILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
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TITLE OF INVENTION: Methods &
FILE REFERENCE: UM-06967
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TYPE: PRT
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Pred. No. 1.6;
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144;

Indels 129;

Gaps

18;

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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Inohara, Nachiro
ITILE OF INUENTION: Methods and Compositions for FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 43
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US-11-317-329-43
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
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LTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL 271
                                                       TARLLIDHGACVDA-QEREGWTPLHLAA--QNNFENVARLLVSRQADPNLRE------
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                                                                                          ----LDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCS
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vo. US20060105413A1
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21.6%; Pred. No. 1.6;
tive 46; Mismatches 144; Indels 12
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US-11-317-329-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
COUNTRY OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nunez, Gabriel
APPLICANT: Inobara, Naohiro
TITLE OF INVENTION: Methods and Compositions
FILE REFERENCE: UM-06967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 765
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                                                                                                                                                                                                                                                                          157
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                                                                                                                                                                                                                                    443 TARLLLDHGACVDA-QEREGWTPLHLAA--QNNFENVARLLVSRQADPNLRE-----
                                                                                                                                                                                                                                                                                                                                                  113 ERTRKTGEAFAAGLAP------DCAITVHTQADTSSPD-----PLFNPLKTGVCQ 156
                                                                                                                                                                                                                                                                                                                                                                                           338 KRALQLSDRKNÍVPRDEELCIYENKVTPLOFIVAQGSVE-----
582 YGASLELPTHQGWTPLHLAAYKGHLEIIHLLAESHANMGALGAVNWT
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TWPVKLGE---LTPRGGELIAYLGHYW-RORLVADGLLPKCGCPQSGQVAII----ADVD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 FLSLLIPLTPQSAFAQSE---PELKLESVVIVSRHGVRAPTKA----TQLMQDVTPDAWP 60
                                                                                                                                                                                                                                                                      ----LDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCS
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                                      ----VTLPT----SVLFIAGHDTNL------ANLGGALELNWT
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                                                                             HLA------VERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYLICKMLLR
                                                                                                                  HNAQFDLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYG---------
                                                                                                                                                          ----AEGKTPLHVAAYFGHVSLVKLLT------SQGAELDAQQRNLRTPL
                                                                                                                                                                                             LTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93.5; DB 7; Pred. No. 1.6;
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RESULT 15
US-10-905-928-150
Sequence 150, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178

al.

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GURRENT APPLICATION NUMBER: US/10/505,928;
CURRENT FILING DATE: 2004-08-27;
PRIOR APPLICATION NUMBER: US 60/363,019;
PRIOR FILING DATE: 2002-03-07;
NUMBER OF SEQ ID NOS: 866;
SOFTWARE: PATCHIN 3.2;
SEQ ID NO 150;
LENGTH: 5738;
TYPE: PATCHING BADIENB
Search completed: June 13, 2006, 10:51:03 Job time : 10.9083 secs
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4.0%; Score 90.5; DB 6; Length 5738;
Best Local Similarity 22.9%; Pred. No. 53;
Matches 110; Conservative 35; Mismatches 159; Indels 177; Gaps
                                                                             2729 Ġ 2729
                                                                                                                                                                                                                                                                                                                  2574 OPRNLTGILVPETGSSNÁYASSFSLOFSSNGLHWHDYRDLL-PGILPLPKVSPÁQGRWGO 2632
                                                                                                                                                                                                                                                                                                                                                                                                 2516 AGLAEGSIHASSQQLEHPTQAALLGAPTQGPSPQGWHAGGDAYAKWHT--RPHYLQLDLL 2573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2489 SC-----CYSPLGL 2515
                                                                                                                                                            2675 L-DPAVW-----TFGRMVQARFVRVWPHDVHHSDVPLQVELLGCEPGVGLRCASGECVLR 2728
                                                                                                                                                                                                                                       2633 QPTMP----FCGFHS------LCPQGPSSVPEGHGLHSMLVEYLLFPRNWDD 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2455 --NQTVQPMA-----TPANAPAPSPQIRFPLAT-----YILPPSGG 2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2419 LTAHCSPYCP--LGS-CPQGWVLVEGTGE-----SCCHCALPGE-----
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                                                                                                                                                                                                                                                                                                                                                               280
                                                                                                                                                                                             363 LSDNSQWIQVSLVFQTLQQMR--DKTPLSLNTPPGEVKLTLAGCEE----RNAQGMCSLA 416
                                                                                                                                                                                                                                                                            313 -VTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPG------GELVFER-WRR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 SIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGA 232
                                                                                                                      417 G 417
                                                                                                                                                                                                                                                                                                                                                                                                                          233 VSLA------SMLTEIFILL-QQAQGMPEPGWGRITDSH-QMNTLLSLHNAQFDLL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFN-PLKTGVCQLDNANVTDAILERAGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 VTPDAWPTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ILIPFLSLLIPLTPQSAF-----AQSEPELKLESVVIVSRHGVR---APTKATQLMQD
                                                                                                                                                                                                                                                                                                                                                           Q-----RTPEVARSRA------TPLLDLIKTALTPHPPQKQAYG----
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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PIR 80:*
1: pir1:*
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3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             June 13, 2006, 10:22:24 ; Search time 25.2661 Seconds (without alignments) 1645.118 Million cell updates/sec
                                                                                                                                                                                                                                                                                            283416 seqs, 96216763 residues
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2258
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                                                                                                                                                                                                                                                      283416
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-17 <DA2>
A;Cross-references: UNIPARC:UPI000016FFB1; GB:S63811; NID:g238656; PIDN:AAB20286.1; PID:

45 96.5				-	40 98.5		38 99		36 99.5	•	-	-		•	_
4.3	4.3	<u>4</u> .	٠.3		4.4	4.4	4.4	4.4	4.4	4.4	4 5	5	5	4.5	4.5
1047	374	328	4056	1034	381	1413	969	560	234	971	425	1387	1214	789	635
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
C85535	139781	A83572	H96599	AB0551	JH0152	D88844	T27997	F84341	F42696	T32883	D83186	A97673	AG2897	AE0064	A45266
	subtilisin (EC 3.4	pyridoxal phosphat	protein F14J16.10	exonuclease SbcC [acid phosphatase (protein ZK792.1 [i	hypothetical prote	hypothetical prote	thrombin (EC 3.4.2	hypothetical prote	hypothetical prote	probable periplasm	conserved hypothet	DNA-directed DNA p	MPL-P protein prec

ALIGNMENTS

A;Accession: A26534 A;Molecule type: DNA A;Residues: 1-50, 'NAGCHPRRMANLAG',65,'T',67-74,'DV',77-111,'S' <tou> A;Residues: 1-50, 'NAGCHPRRMANLAG',65,'T',67-74,'DV',77-111,'S' <tou> A;Residues: 1-80, 'NAGCHPRRMANLAG',65,'T',67-74,'DV',77-111,'S' <tou> A;Cross-references: UNIPARC:UPI000016BDB2; GB:X05471; NID:g40925; PIDN:CAA29031.1; PID:g/ R;Dassa, J.; Fsihi, H.; Marck, C.; Dion, M.; Kieffer-Bontemps, M.; Boquet, P.L. Mol. Gen. Genet. 229, 341-352, 191 Mol. Gen. Genet. 229, 341-352, 191 A;Title: A new oxygen-regulated operon in Escherichia coli comprises the genes for a put A;Title: A new oxygen-regulated operon in Escherichia coli comprises the genes for a put A;Reference number: S17958; MUID:92049231; PMID:1658595 A;Accession: S17960 A;Status: not compared with conceptual translation</tou></tou></tou>	A;Accession: B44839 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Rosidues: 1-432 <blat> A;Cross-references: UNIPARC:UPI00004750A; GB:AE000200; GB:U00096; NID:g2367111; PIDN:AAC A;Experimental source: strain K-12, substrain MG1655 A;Experimental source:</blat>	Rightener, K.; Jany, K.D. Biol. Chem. Hoppe-Seyler 372, 664-665, 1991 A;Title: Characterization of a phytase from Escherichia coli. A;Reference number: S18018 A;Accession: S18018 A;Molecule type: protein A;Residues: 23-33 cGRE> A;Cross-references: UNIPARC:UPI0000179815 A;Cross-references: UNIPARC:UPI0000179815 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503	RESULT 1 B36733 B36733 acid phosphatase (EC 3.1.3.2) precursor - Escherichia coli (strain K-12) N;Alternate names: phosphoanhydride phosphohydrolase, periplasmic; phytase 6 C;Species: Escherichia coli C;Date: 19-Apr-1991 #sequence revision 19-Apr-1991 #text change 09-Jul-2004 C;Accession: B36733; S18018; B64839; A26534; S17960; S33278 R;Dases, J.; Marck, C.; Boquet, P.L. J. Bacteriol. 172, 5497-5500, 1990 A;Title: The complete nucleotide sequence of the Escherichia coli gene appA reveals sig. A;Reference number: A36733; MUID:90368616; PMID:2168385 A;Accession: B3673 A;Accession: B36733 A;Status: preliminary A;Rolecule type: DNA A;Residues: 1-432 cDAS> A;Cross-references: UNIPROT:P07102; UNIPARC:UPI000004750A; GB:M58708; NID:g145283; PIDN D;Cross-references: UNIPROT:P07102; UNIPARC:UPI000004750A; GB:M58708; NID:g145283; PIDN	

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RESULT 2
H90770
phosphoanhydride phosphorylase [imported] - Bscherichia coli (strain O157:H7, substr C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90770
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Ccession: H90770
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:08XC29; UNIPARC:UPI0000D0517; GB:BA000007; PIDN:BAB3455
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Greiner, R.; Konietzny, U.; Jany, K.D. Arch. Biochem. Biophys. 303, 107-113, 1993 A;Title: Purification and characterization A;Reference number: S33278; WUID:93256556; A;Accession: S33278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: monomer; periplasmic space; phosphohistidine; phosphoprotein; F;1-22/Domain: signal sequence #status predicted <SIG> F;23-112/Product: acid phosphatase #status predicted <MAT> F;38/Active site: Arg #status predicted F;38/Active site: His (phosphohistidine intermediate) #status predicted
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A; Residues: 23-31,'A', 33-34 <GR2>
A; Crooss-references: UNIPARC:UPI0000179816
C; Comment: In addition to CAMP-mediated co
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Pred. No. 2e-167;
0; Mismatches 8;
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glas iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein appA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: D85633
                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q8XC29; UNIPARC:UPI0000165751; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Genome sequence of A,Reference number: A85480; A,Accession: D85633 A,Status: preliminary
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A;Gene: ECs1136
                                                                                                                                                                                                                                                                        A;Gene:
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A; Residues: 1-444 <STO>
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Best Local Similarity
Matches 419; Conserv
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Best Local
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GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFT 178
                                                                                                                                     MKAILIPFLSLLIPLTPQSAFAQS--EPELKLESVVIVSRHGVRAPTKATQLMQDVTPDA
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                                                                   WPTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKT 118
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Pred. No. 2.3e
0; Mismatches
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                                                                                                                                                                                          Score 2144; DB 2;
Pred. No. 2.4e-164;
"""matches 13;
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2.3e-164;
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RESULT 4

AC0201

AC0201

acid phosphatase (EC 3.1.3.2) [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0201
C;Accession: AC0201
C;Accession: A. Mren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, P.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Davies, P.; Dougan, (deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, (deno-Tarraga, A.M.; Chillingworth, T.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
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                                                    TPHPPQKQAYGVTLPTS----VLFIAGHDTNLANLGGALBLNWTLPGQPDNTPPGGELVF
                                                                                     PFAQMGDVLNFAASPYCKSLQQQGKTCDFAHFAANEVNVNKEGTKVTLSGPLALSSTLGE
                                                                                                                                                                                                                              DGVAPGCGLTVHNQADLKKTDPLFHPVEAGVCKLDAAQTDKAIEEQLGGPLDTVSQRYAK
                                                                                                                                                                                                                                                           AGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILBRAGGSIADFTGHYQT
                                                                                                                                                                                                                                                                                                 VKAGYLTPRGAELVTLMGGFYGDYFRSLGLL-AAGCPAEGGVYAQADIDQRTRLTGQAFL
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46.1%; Pred. No. 3.3e-69;
ative 67; Mismatches 153;
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bugan, G.;
Barrell,
periplasmic glucose-1-phosphatase [imported] - Esch C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: B85636 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau,
                                                                                        RESULT
B85636
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R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyan gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagav DNA Res 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   periplasmic glucose-1-phosphatase [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: F90773
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A;Molecule type: DNA
A;Residues: 1-413 <HAY>
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Best Local Similarity
Matches 141; Conserv
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LNEA 411
                                                                                                                                  PRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDC
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                                 VNEA
                                                                   DSKANRDLMKIEYVYÓSAEÓLRNADALTLOAPAORVTLELSGC-PIDADGFCPMDKFDSV
                                                                                               RLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEBRNAQGMCSLAGFTQI
                                                                                                                                                                                                                                     AQGMP---BPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTALTPHP
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                                                                                                                                                                                                     YEGFPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL----
                                                                                                                                                                                                                                                                       LEKI VNYKDSPAC----KEKQQCSLVDGKNTFSAKYQQEPGVSGPLKVGNSLVDAFTLQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.8%; Score 560; DB 2;
ilarity 33.3%; Pred. No. 3.7e-37;
Conservative 73; Mismatches 174
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V.; Mau, B.; Glasner,

J.D.; Rose,

D.J.;

Mayhew

Escherichia coli

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#text_change 09-Jul-2004

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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: B85636

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-413 - C5TO>

A;Residues: 1-413 - C5TO>

A;Residues: UNIPROT:Q8XBZ6; UNIPARC:UPI0000D0533; GB:AE005174; NID:g12514273;
A;Genetice: Gpp
A;Cross-references: UNIPROT:P19926; UNIPARC:UPI00001256FB; GB:M33807; NID:g145217; R;Blattuer, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64841
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-413 <BLAT>
                                                                                                                                                                                                                                                    glucose-1-phosphatase (EC 3.1.3.10) precursor - Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_chan;
C;Accession: JV0087; H64841
R;Pradel, E.; Marck, C.; Boquet, P.L.
J. Bacteriol. 172, 802-807, 1990
A;Title: Nucleotide sequence and transcriptional analysis of A;Reference number: JV0087; MUID:90130318; PMID:2153660
A;Accession: JV0087
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A;Residues: 1-413 <P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVLLASNAQAQTVPEGYQLQQVLMMSRHNLRAPLANNGSVLEQSTPNKWPEWDVPGGQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPLTPQSAFAQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAMPTWPVKLGELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQI 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQKQAYGVTLPTS---VLFIAGHDTNLANLGGALELN-WTLPGQPDNTPPGGELVFERWR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEGFPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQGMP--EPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTALTPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEKI VNYKDSPAC----KEKQQCSLVDGKNTFSAKYQQEPGVSGPLKVGNSLVDAFTLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIPVHHQEKMGTMDPTFNPVITD----DSAAFSEQAVAAMEKELSKL-QLTDSYQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AITVHTQADTSSPDPLFNPLKTGVCQLDNANVTD---AILERAGGSIADFTGHYQTAFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%;
ilarity 33.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 560; DB 2; Length 41
Pred. No. 3.7e-37;
73; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                             07-Sep-1990 #text_change 09-Jul-2004
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A;Description: essential for growth in a high-phosphate medi A;Note: optimal at low pH
G;Keywords: homodimer; periplasmic space; phosphohistidine;
F;1-22/Domain: signal sequence #status predicted <SIG-
F;23-413/Product: glucose-1-phosphatase #status predicted <N
F;40/Active site: His (phosphohistidine intermediate) #status
F;311/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI00001256FB; GB:AE000202; GB:U00096; NID:g1787233; PIDN:AA(A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: agp
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C; Function:
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Best Local
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LNEA
                                    VNEA
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                                                                      DSKANRDLMKIEYVYÓSAEÓLRNADALTLOAPAORVTLELSGC-PIDADGFCPMDKFDSV
                                                                                        RLSDNSQWIQVSLVFQTLQQMRDKTFLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQI
                                                                                                                                                                                                            YEGFPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL----
                                                                                                                                                                                                                                                AQGMP--EPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTALTPHP
                                                                                                                                                                                                                                                                                                                  LERVINFPQSNICLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQ
                                                                                                                                                                                                                                                                                                                                                       DIPVHHQEKMGTMDPTFNPVITD----DSAAFSEQAVAAMEKELSKL-QLTDSYQL----
                                                                                                                                                                                                                                                                                                                                                                                                                             TKGGVLEVYMGHYMREWLAEQGMVKSGECPPPYTVYAYANSLQRTVATAQFFITGAFPGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVILASNÁQÁQTVÞEGYQLQQVLMMSRHNLRÁÐLANNGSVLEQSTÐNKWÞEWDVÞGGQLT
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                                                                                                                                                                         PQKQAYGVTLPTS---VLFIAGHDTNLANLGGALELN-WTLPGQPDNTPPGGELVFERWR
                                                                                                                                                                                                                                                                                    LEKI VNYKOSPAC-
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 411
                                                                                                                                        -VTDRTSAPKITVLVGHDSNIASLLTALDFKPYQLHDQNERTPIGGKIVFQRWH
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--KEKQQCSLVDGKNTFSAKYQQBPGVSGPLKVGNSLVDAFTLQY
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Pred. No. 1.1e-36;
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Salmonella

enterica

Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov. glucose-1-phosphatase precursor (GIPase), secreted [imported] - C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AG0632 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd A; Cross-references: C; Genetics: A; Molecule type: DNA A; Residues: Status: preliminary 1-413 <PAR> UNIPARC: UPI0000059FE6; GB:AL513382; PIDN:CAD08242.1; PID:g16502289; N.R.; Pickard, ies, R.M.; Dowd, 18-Nov-2002 D.; Wain, J.; Cl, L.; White, N.; Churcher,

A;Gene:

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A;Gene: agp (C;Keywords: periplasmic space; phosphohistidine; phosphoprotein; F;1-29/Domain: signal sequence #status predicted <SIG>F;30-417/Product: glucose-1-phosphatase #status predicted <MAT>F;42/Active site: His (phosphohistidine intermediate) #status preficted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
$25627
$25627
$glucose-1-phosphatase (EC 3.1.3.10) precursor - Providencia rettgeri
C;Species: Providencia rettgeri
C;Species: Providencia rettgeri
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: $25627
C;Accession:
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C;Genetics:
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A; Residues: 1-417 < RIC>
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Matches 138
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                                                                                                                                                                                                                                                                                                              Similarity
KVTVLVGHDSNIASLLTALDFKFYQLHDQYBRTFIGGQLVFQRWHDGNANRDLMKIEYVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAWPTWPVKLGELTPRGGELIAY
                                                                AGAFFGCKVNIHHQFEIGKMDFVFNFIIT-----
                                                                                            AGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTG--HY
                                                                                                                                        TTQGGALEVYMGHYFREWIDQNKLLADEL----CPTSNEDIYLYTNSLQRTIATAQFFA
                                                                                                                                                                      TPRGGELIAYLGHYWRQ-----RLVADGLLPKCGCPQSGQ-VAIIADVDERTRKTGEAFA 123
                                                                                                                                                                                                                  ALFAPIAPTMASTDNQADMVLDQVLVLSRHNLRTPIVNTGILTEVTDKKWPDWDAKSGYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGHYTREWLVAQGLIPSGECPAPDTVYAYANSLQRTVATAQFFITSAFPGCDIPVHHQEK 141
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                            23.8%; Score 538; DB 2; 30.4%; Pred. No. 2.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.2%; Score 547; DB 2; 33.7%; Pred. No. 4.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.; Lombardi, G.; Satta,
Library, September 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                            Mismatches 175;
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                                                            -NGSPEFKQKALAAMDDYLKGLSL
                                                                                                                                                                                                                                                                                                                              Length 417,
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-414 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                periplasmic phosphoanhydride phosphohydrolase [imported] - Caulobacter cres C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: E87316
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nes 145; Conserv
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                    LAGETQIVNEA 425
                                                                            LVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCS 414
                                                                                                                                                                        LIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG-QPDNTPPGGE 354
                                                                                                                                                                                                                                                                                                                            RELERVINFPQSNLCLKREKQDESCSLTQALPSELKV-----SADCVSLTGAVSLA
                                                                                                                                                                                                                                                                                                                                                                                                    LAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGHYQTAF
                                                            LVFERWRR-DDGVRVVRVRFTGQSLSQLRNMTALDAKTPPLSAPVFVQGCGTATPAFDCR
                                                                                                                                    RLAATLR----DGAAAIG-PVDARLVIIAGHDGTLASLGGLLRMEWTLPGYQPNQIQPGGA
                                                                                                                                                                                                              SGVTESLLMAWADGRDFAGLGWKSLDEBALTRSFFLHQAEFDLRLRTPYVARTLAGHLAD
                                                                                                                                                                                                                                                  SMLTEIFLLQQAQGMPEPGWG-RITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLD
                                                                                                                                                                                                                                                                                          EQLDALLMQCDKGPC--
                                                                                                                                                                                                                                                                                                                                                                  LAPGCPVTVNTVGE-GNIDPMFEPVKAGIVKADHALARAAVAGRVGGDLTAWSASHNQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTRIAVVTLATASAGAASAB--TLEKVVILSRHGVRSAMSSPERLEEASARPWPRFEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSL---LIPHTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFLLQQAQGMP--EPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.7%; Score 536; DB 2; 33.6%; Pred. No. 3.1e-35; tive 62; Mismatches 186
                                                                                                                                                                                                                                                                                          ---PPAPGKRRVFDAKPGFVDGEBLAGLSGPEAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186;
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acid phosphatase (BC 3.1.3.2) ACP2 precursor [validated] - human N;Alternate names: acid phosphatase, lysosomal C;Species: Homo sapiens (man) C;Date: 04-Dec-1992 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004 C;Accession: S06167; S05525; S01155
A;Reference number: S06167
A;Accession: S06167
A;Molecule type: DNA
A;Residues: 1-423 < VON>
                                                                            submitted to the EMBL Data Library,
                                                                                            R; von Figura, K.
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C; Superfami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid
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C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                   RESULT 12
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;Accession: T16058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAIL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTGKDNRTSASAQAMFAGFLPP-----NEDQTWNYELKWQPV------AQLTDESI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----FISGHDTNLVTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AWPTWPVKLGELTPRGGELIAYLGHYWRQRL-----VADGLLPKCGCPQSGQVAI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRLVLLLF--FLFPV----AFG-----KLKFVQIWFRHGERTPGHYLYFPGDDLNNVDY 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59/3; 88/3; 138/3; 202/3; 244/1; 270/3; 312/3; 349/3; 377/1
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21.7%; Pred. No. 0.0035;
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                                                                            June 1989
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A;Description: catalyzes the hydrolysis of a wide range of phosphate esters C;Superfamily: mammalian acid phosphatase C;Keywords: glycoprotein; phosphoistidine; phosphoprotein; phosphoric monoester hydrolase; F;1-30/Domain: signal sequence #status predicted <SIG>
F;31,423/Product: acid phosphatase ACP2 #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Pohlmann, R.; Krentler, C.; Schwaut, D., Commun. R;Pohlmann, R.; Krentler, C.; Schwaut, D., Casteller, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P11117; UNIPARC:UPI0000131FE1; R;Geier, C.; von Figura, K.; Pohlmann, R. Biochem. 183, 611-616, 1989

A;Title: Structure of the human lysosomal acid phosphatase A;Reference number: S05525; MUID:89377828; PMID:2776754
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A;Cross·references: GDB:118963; OMIM:171650
A;Map position: 11911.2-11p11.11
A;Introns: 38/3; 70/3; 99/3; 150/3; 183/3; 213/3;
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A; Residues: 1-423 < POH>
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A; Residues: 1-29 < GEI>
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;42/Active site: His (phosphohistidine intermediate) #status predicted 
;42/Active site: His (phosphohistiding site: carbohydrate (Asn) (coval 
;92,133,167,177,191,267,322,331/Binding site: carbohydrate (Asn) (coval 
;159-370,212-310,345-349/Disulfide bonds: #status predicted
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                                                                      VSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIP
                                                                                                                                                     ---LP-KLLVYSAHDTTLVALQMALDVY
                                                                                                                                                                                                                            GVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVPERWRRLSDNSQWIQ 371
                                                                                                                                                                                                                                                                                                       PW---ASPOTMORLSRLKDFSFRFLFGIYQQAEKARLQGGVLLAQIRKNLTLMATTSQ--
                                                                                                                                                                                                                                                                                                                                                                          GWGRITDSHQWNTLLSLHNAQFDLL---QRTPEVARSRATPLLDLIKTALTPHPPQKQAY
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   -RNESDKAPWPLSLP-----
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23.3%;
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Pred. No. 0.009
43; Mismatches
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-GCPHR----
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0.0091;
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   -CPLQDFLRL-TEPVVP
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acid phosphatase (EC 3.1.3.2) precursor - C;Species: Rattus norvegicus (Norway rat) C;Date: 29-Jan-1990 #sequence_revision 29-C;Accession: A33395

- rat (t) 29-Jan-1990

#text_change 09-Jul-2004

A33395

RESULT

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acid phosphatase (EC 3.1.3.2) Acph-1 precursor, C;Specias: Drosophila melanogaster C;Date: 06-Dec-1996 #sequence revision 06-Dec-19 C;Accession: $64682; $64681 R;Chung, H.J.; Shaffer, C.; MacIntyre, R. Mol. Gen. Genet. 250, 635-646, 1996
                                                                                                                                                                                             Mol. Gen. Genet. 250, 635-646, 1996
A;Title: Molecular characterization of the lysosomal acid A;Reference number: S64681; MUID:96194627; PMID:8676866
A;Accession: S64682
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                  A;Cross-references: UNIPARC:UPI000017595EC;Genetics:
                                                      A; Molecule type: mRNA
A; Residues: 1-31,'Y', 33-438 < CHW>
                                                                                                     A; Cross-references: A; Accession: S64681
                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-438 < CHU>
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A;Title: Isolation and sequencing of a cDNA clone encoding A;Reference number: A33395; MUID:89350910; PMID:2764916
A;Accession: A33395
A;Status: preliminary
                                                                                      A; Status: not compared with
                                                                                                                                                                             A;Status: not compared with
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A; Residues: 1-423 < HIM>
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Best Local S
Matches 102
FlyBase:Acph-1
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                                                                                                                          UNIPROT: Q9VADO;
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                                                                                      conceptual
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Pred. No. 0.16,
46; Mismatches
                                                                                                                          UNIPARC: UPI000017595D
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RESULT 15
S14742
                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P24638; UNIPARC:UPI0000027103; C;Superfamily: mammalian acid phosphatase C;Keywords: lysosome; phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                               RiGeier, C.; von Figura, K.; Pohlmann, R.
Biol. Chem. Hoppe-Seyler 372, 301-304, 1991
A;Title: Molecular cloning of the mouse lysosomal acid A;Reference number: S14742; MUID:91282986; PMID:2059337
A;Accession: S14742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid phosphatase (BC 3.1.3.2) precursor - mouse (f: C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0000032
C;Superfamily: mammalian acid phosphatase
C;Keywords: phosphoric monoester hydrolase
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-438/Product: acid phosphatase Acph-1 #status predicted <MAT>
문
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-421 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S14742
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                                                                                                                                                                                                                                                    Query Match
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Best Local
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                                                                                                                                            œ
                                                                                                                                                                          2 KAILIPF-----LSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTP
                                                                                                                                                                                                                  l Similarity
98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
LMSAEANLAGLFPP-----NEVQHFSPNISWQPI-----PVHTVPITE
                                RKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIA 175
                                                                                                                                          QAALLQFLLGMCLTVMPPIQARS
                                                                    YQEEKWPQGFGQLTKEGMLQHWELGQALRQRY--HGFL---NTSYHRQEVYVRSTDFDRT
                                                                                                      DAWPTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVD-ERT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYNWTLPKWTKKVYGREELTYVS--NFAPAISSYTRKLARLKAGPLLKDIFQRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YTACIMMELRVDETNTPLVSIFYKNTTAEPLPLDIFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWOPIPIHTSPEREDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGHYQTAFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSQWIQVSLVFQTLQQMRDKTPL----SLNTPPGEVKLTLAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEKSSGSLKPDRSMWVYSAHDTTVASVLNALKL-FEL-----HSPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKQAYGVTLPTSVLFI-AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLL-DLIKTALTPHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LERVINFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKWLRNRY--SNLLPPI---YSNENIYVQSTDVDRTLMSAQSNLAGLYEPQGEDIWNTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHYWRORLVADGLLPKCGCPQSGQVAIIADVD-ERTRKTGEAFAAGL----APDC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLKFVHVIYRHGDRTPV------DPYPTDPWGDRKFWPTGWGDLTNLGKQEHYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LASLESSPERK-ALTEKHRNLFAYLSEKGGRPVKTFID------AQYLNNTLFIEN
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                4.9%; Score 111.5; 1
21.4%; Pred. No. 0.4;
vative 53; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                      monoester hydrolase
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Pred. No. 0.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.35;
                                                                                                                                          LREVTLLYRHGDRSPVKT----YPKDP
                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                Indels 137;
                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatase
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176 DPTGHYQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSL 235
u m m v 4 - 1 m u

Search completed: June 13, 2006, 10:29:30 Job time: 26.2661 secs

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Result
No.
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:

-MODEL-frame+ p2n.model -DEV-xlh
-Q-|abss/ABSSWEB =pool/US10601319/runat 12062006 180050 27480/app query.fasta 1
-Q-|abss/ABSSWEB =pool/US10601319/runat 12062006 180050 27480/app query.fasta 1
-DB=GenEmbl -QFMT-fastap -SUFFIX=ye -MIMMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs06h
-USER=US10601319 @CGN 1 1 3991 @runat 12062006 180050 27480 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPD=10 -XGAPEXT=0.5 -FGAPEPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on:
                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                         Score
     2182
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seq length:
                                                                                                                                                                                                                             GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_pl:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
11: gb_ov:*
12: gb_nts:*
13: gb_in:*
14: gb_om:*
                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xgapop 10.0 , y
Ygapop 10.0 , y
Fgapop 6.0 , E
Delop 6.0 , I
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2258
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96.6
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Ygapext
Fgapext
Delext
       NNN
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   AR636190
AR636191
AX356572
                                                                           Ħ
                                                                                                                               SUMMARIES
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8030.264 Million cell updates/sec
AR636190 Sequence
AR636191 Sequence
AX356572 Sequence
                                                                       Description
                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
AR636190
LOCUS
                                    Score:
                                                                                                          ORIGIN
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JOURNAL
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ALIGNMENTS

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Percent Similarity:
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                                                                                                                                source
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AR636190
AR636190.1
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Short,J.M., Kretz,K.A., Gray,K.A., Barton,N.R.,
O'Donoghue,E. and Mathur,E.J.
O'Donombinant bacterial phytases and uses thereof
Patent: US 685365-A 7 15-FEB-2005,
Diversa Corporation, San Diego, CA
Location/Qualifiers
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from patent US 6855365.
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          PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
                                                      LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                                                   ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
                                                                                                                                                AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
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                                                                                       CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTTGATCAAGACAGCG
                                                                                                                                   GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                                                                                                               GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC
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Sequence 9
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Short,J.M., Kretz,K.A., Gray,K.A., Barto
O'Donoghue, B. and Mathur, E.J.
O'Combinant bacterial phytases and uses
Patent: US 685365-A 9 15-FEB-2005;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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RESULT 3
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Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                    TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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                       CTTAMACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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Recombinant bacterial phytases and uses
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stem_loop 118149 /gene="appA" -35_signal 133138 /gene="appA"	/ gene="appx" /note="notes" / codon start=1 / trans1 table=1 / product="unknown" / protein id="AAA72085.1" / db xref="g1:145284" / translation="MWYLLWFVGILLMCSLSTLVLVWLDPRLKS"	RBS 38 /gene="appA" CDS 16108	/or /mo /db 3.	AL ED S	Escherichia coli acid phosphatase AL J. Biol. Chem. 267 (32), 22830-22836 (1992) ED 1429631 CE 3 (sites) CE 3 (sites) RS Ostanin,K. and Van Etten,R.L.	Kuciel,R.,	Enterobacteriaceae; Escherichia. REFERENCE 1 (bases 1 to 1901) AUTHORS Dassa,J., Marck,C. and Boquet,P.L. The complete nucleotide sequence of the Escherichia coli gene reveals significant homology between pH 2.5 acid phosphatase qlucose-1-phosphatase	M58708.1 GI:145283 Escherichia coli Escherichia coli Bacteria; Proteobacteria; Gammaproteobacteria;	RESULT 5 ECOAPPAA ECOAPPAA LOCUS ECOAPPAA 1901 bp DNA linear BCT 04-APR DEFINITION Escherichia coli periplasmic phosphoanhydride phosphohydrolase (appA) gene, complete cds. ACCESSION MS8708	Qy 401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln	Qy 381 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr	Db 1208 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTTGTTGAACGCTTGG Qy 361 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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Forsberg,C.W., Golovan,S. and Phillips,J.P.
Transgenic animals expressing salivary proteins
Patent: WO 0064247-A 5 02-NOV-2000;
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                                                                                                                                    CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC
                                                                                                                                                  GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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                   LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
                                                                                                                                   TCCAGTCCCGATCCCTTATTTAATCCTCTAAAAACTGGCGTTTTGCCAACTGGATAACGCG
                                                                                                                                               SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
                                                                                                                                                                                                                                  GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
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         CTTAAACGTGAGAAACAGGAAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                   CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                             TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                           AACGTGACTGACGCGATCCTCAGCAGGGCGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                       AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
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/mol type="unassigmed DNA"
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321 PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	281 ArgThrProGlivalAlaArgSerargA.aThrProGuueuAspueuileuysIntala 300	61 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln	241 GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr 260	221 LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	201 LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220 	181 TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200 	161 AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180 	141 SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160	121 AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140	101 GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120	81 GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro 100	61 ThrTrpProVallysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80	41 ValargalaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	21 PheAlaGlnSerGluProGluLeuLyBLeuGluSerValValIleValSerArgHiBGly 40 	1 MetLysalaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla 20 	2 Gaps: 0 601-319-10 (1-432) x AX042375 (1-6116)

81 GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro 	Oy 41 ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	21 PheAlaGlnSerGluProGluLeuLysLeuGluSerValValILeValSerArgHisGly 	1 MetlyalaileLeuileDrop	Match: 96.6% Indels: 2 Gaps: -601-319-10 (1-432) x AX042373 (1-6708)	Alignment Scores: 2.37e-195 Length: 6708 Score: Percent Similarity: 98.18 Conservative: Best Local Similarity: 98.18 Mismatches: 8	/noTe="R15/APPA + intron plasmid with pBLCAT3 vector"	rce	c animals expressing salivary pro 0064247-A 2 02-NOV-2000; Y OF GUELPH (CA) Location/Oualifiers	ORGANISM synthetic construct other sequences; artificial sequences. REFERENCE 1 AUTHORS Forsberg.C.W. Golovan.S. and Dhilling.T b		RESULT 9 AX042373 AX042373 AX042373 From Patent WOOD64247 DEFINITION Sequence 2 from Patent WOOD64247	QY 421 IleValAsnGluAlaArgIleProAlaCy8SerLeu 432	401 Le 3011 CT	Qy 381 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400	Qy 361 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380	Db 2831 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 2890
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10 78 AX042378 17732 bp DNA linear PAT 23-NOV-2000 TION Sequence 7 from Patent WO0064247. ION AX042378 N AX042378.1 GI:11340996	3011 CTGGCAGGATGTGAAAAGCACGCATACCCGCTTGCAGTTTG 3106		361 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380 	341 ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp 360 	321 PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp	301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320	281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300	261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln 280 	241 GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr 260	221 LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	201 LeuLyBArgGluLySGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220	181 TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200 	161 AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180 	141 SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160 	121 AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140 	

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                                                                                                                                                                                                     AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
                                                                                                                                                                                                                                                                                                    GlyHisTyrTrpArgGinArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                                                                                                                                                                                                                                                                                                                            ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                      ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
                                 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                            LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
                                                                          CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                     TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                                                   AACGTGACTGACGCGATCCTCAGCAGGGCAGGGCAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                                               AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                                                                                                                                                             TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                                                                                                                                                         SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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/noTe="Lama2/APPA transgene"
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UThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLe 	roGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAl 	pSetHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln 	GluilePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgileTh 	lSerAlaAspCy8ValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuTh 	eulysargGluLysGlnaspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 	TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCy CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTG	AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAs; ACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGA	PrProAspProLeuPhe	.aPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 	InSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 	lyHisTyrTrpargGlnArgLeuValAlaAspGlyLeuLeuProLysCysGl: ACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGG	ProVallysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAl CGGTAAAACTGGGTTGGCTGACACCGCGGTGGTGAGCTAATCGC	7	lnSerGluProGlu AGAGTGAGCCGGA(MetLysAlaIleLeuIleProPheLeuSerLeuIleProLeuThrProGlnSerAl	15	2182 98.1
1LysGlnAlaTyr AAACAGGCGTATV :AsnLeuAlaAsnl	JSerArgAlaThr] AGCCGCGCCACC	LeuLeuSerLeui TTGCTAAGTTTG	NAlaGlnGlyMet GCACAGGGAATG	SerLeuThrGly/ TCATTAACCGGTO)GluSerCysSer1 GABAGCTGTTCA	LeuGluArgVall	nGluArgAlaGlyd AGCAGGGCAGGA	AsnProLeuLys! AATCCTCTAAAA	\ProAspCysAla: \CCTGACTGTGCAJ	:IleAlaAspVal <i>l</i> ATTGCTGATGTCC	JLeuValAlaAsp(CTGGTAGCCGACK	GluLeuThrProA	ThrGlnLeuMeto	LeuLysLeuGlus CTGAAGCTGGAAJ)PheLeuSerLeuI TTTTATCTCTT)]	Matches: Conservat
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Short, J.M., Kretz, K.A., Gray, K.A., Ba
O'Donoghue, E. and Mathur, E.J.
Recombinant bacterial phytases and us
Patent: US 6855365-A 5 15-FEB-2005;
Diversa Corporation, San Diego, CA
Location/Qualifiers
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Sequence
AR636188
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LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
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                                                                                                                                                                                                                                                                                                                                                                                                IleValAsnGluAlaArgIleProAlaCysSerLeu
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patent US 6855365.
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LeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 38 	361 ArgArg	. н
ProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp 3 	341 ThrLeu 208 ACGCTT	н
AlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 3 	321 Phelle. 148 TTTATC	н
ProHisproProGlnLysGlnAlaTyrGlyValThrLeuproThrSerVa 	301 LeuThr	<u>.</u>
ProGluvalalaargSerargAlaThrProLeuLeuAspLeuIleLysTh 	281 ArgThr	μ
HisGlnTxpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuC 	61 AspSer	
ePheLeuLe	41 GluIle 08 GAGATA	
SerAlaAs \GCGCCGA	21 LysVal	
SATGGluLyBGlnAspGluSerCyBSerLeuThrGlnAlaLeuProSerGluLeu 220 	01 LeuLys. 88 CTTAAA	
laph CGTT	81 TyrGln	
SACGO	69	
rProAspPr CCCGATCO	41 SerSer 08 TCCAGT	
9AlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAs 	Alaphe	
lyglnva grcaggr	01 Glns 88 CAG	
BTYrTrpAr TACCAACG	81 GlyF 28 GGAG	
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gAlaProThrLysAlaThrGlnLeuM 	Vala GTGCX	
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1448 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1483	421 IleValAsnGluAlaArgIleProAlaCysSerLeu 432	1388 CTGGCAGGATGTGAAGAGCGAAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1447	401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420	

Search completed: June 14, 2006, 13:55:38 Job time: 5313.22 secs

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-MODEL-frame+ p2n.model -DEV-xlh
-Q-/abss/ABSSWEB spool/US10601319/runat_12062006_180047_27417/app_query.fasta_1
-Q-/abss/ABSSWEB spool/US10601319/runat_12062006_180047_27417/app_query.fasta_1
-DB=N Geneseq -QFMT-fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALICN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10601319_@CGN 1_1 749_@runat 12062006_180047_27417 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -SARPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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CDS US2005246780-A1 Synthetic. Escherichia coli; strain K12 Transgenic animal; gene therapy; feedstuff; food; thermostable; mutant; ds; coding sequence; 3-phytase; recombinant DNA; appA gene. Escherichia coli phytase appA mutant DNA SEQ ID NO: 1 #1. 29-DEC-2005 (first entry) partial Location/Qualifiers product= "Bscherichia coli phytase mutant protein" note= "No stop codon" EC_number= "3.1.3.8" *tag= . .1296

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01-MAR-1999;
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24-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also useful in gene therapy and in production of transgenic animals. The present sequence is the SEQ ID NO: 1 which is given in the sequence listing. This sequence differs from the SEQ ID NO: 1 shown on page 19 in disclosure of the specification (see AED50824).
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Mathur EJ;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated or recombinant nucleic acid encoding as foodstuff, and for oil degumming, producing an a phytase enzyme supplement to an animal.
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GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                           ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
                                                                                                                               TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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                                                                                         CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                         LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
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The invention discloses a new isolated or recombinant nucleic acid which concleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic conveleic acid, an antisense oligonuclectide, inhibiting the translation of a second domain, an array comprising immobilised polypeptide and cell, a heterodimer comprising the polypeptide and second domain, an array comprising immobilised polypeptide or nucleic colid, a hybridoma comprising an antibody that specifically binds to the polypeptide, a food supplement for an animal, an edible enzyme delivery matrix, an edible pellet comprising a granule edible enzyme delivery colypeptide, making an anti-phytase antibody, producing a recombinant conformation, a soybean meal, isolating or identifying the polypeptide, making an anti-phytase antibody producing a recombinant conformation or the metabolic flux analysis, increasing conformation or the resistance or thermostability of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a consitul and processing of corn and sorghum kernels. The phytase activity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytase rich ingredients or encoding the modified Escherichia coli phytase.
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000; 20
24-MAY-2001; 20
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improving the feeding value of phytate rich ingredients or as an aid
phytate digestion.
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Best Local Similarity:
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product= "Mutant phytase"
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24-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as guppy, zebrafish, molly, swordtail, CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BART/) BARTON N R. (GARR/) GARRETT J B. (ODON/) O'DONOGHUE E. (MATH/) MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1308 BP; 315 A; 345 C;
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Mather EJ;
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                   AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr
                                                                      GlnSerGlyGlnValAlaIleIleAlaAepValAepGluArgThrArgLyeThrGlyGlu
                                                                                                            GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG
                                                                                                                              GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                                                                                                                                                                  ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGluCeuIleAlaTyrLeu
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AEE75420 DNA; 1308

AEE75420;

(first entry)

E. coli B modified appA phytase 819PH59 DNA sequence SEQ 占 ĕ

ds; coding sequence; mutant; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture;

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Alignment Scores: Pred. No.:
                                                                               of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition; a kit; an immobilized phytase; a fertilizer or soil additive; a liquid complement for preventing muscle cramps; a hydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing pollution and increasing culturent availability in an environment or environmental sample by complement useful for treating, preventing or reversing osteoporosis or cupilement useful for treating, preventing or reversing osteoporosis or complementing muscle cramps. The liquid supplement is useful for preventing muscle cramps. The novironment or environmental complement or environmental sample by degrading environmental phytic acid, where the environmental complement or environmental sample comprises a soil or a body of water. The immobilized comprises a soil or a body of water the immobilized phytase is useful in foodstuffs for improving the feeding value of phytate rich ingredients.
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01-MAR-1999;
13-APR-1999;
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                                                     Sequence 1308
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25-MAY-2000;
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) BARTON N R.
) GARRETT J B.
) ODONOGHUE E.
BAUM W.
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2001US-00866379.
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99US-00291931.
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3.47e-202
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                                                         LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                                                                                                                                GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA
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 PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
                                                                                                           CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
                                       TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGACATTACCCACTTCAGTGCTG
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pharmaceutical;
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ical; fertilizer; cran
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replace(439,A)
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replace(470,G)
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replace(438,A)
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  01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
The present sequence is that of a polynucleotide encoding a novel modified phytase derived from the Escherichia coli appA protein, with improved thermal tolerance and protease stability compared to the wild-type. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, where the polypeptide is a modified sequence (AEE75421) derived from the Escherichia coli K-12 appA
                                                                                Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
                                                                 Claim 1; Page; 82pp; English.
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(ODON/)
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(GRAY/)
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(ROBE/)
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DB; AEE75421.
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOCHUE E.
                                                                                                                                                                              BAUM W.
ROBERTSON
ZORNER P.
                                                                                                                                                  , Kretz KA,
Robertson DE,
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2000US-00580515.
2001US-00866379.
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CC phytase (AEE75419). The modification of the enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of CC the protein. The specification also claims a pharmaceutical composition; CC a kit; an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising CC the novel phytase, and a method of reducing pollution and increasing cC nutrient availability in an environment or environmental sample by CC degrading environmental phytic acid. The novel enzyme is a dietary supplement useful for treating, preventing or reversing osteoporosis or cc bone loss, and preventing muscle cramps. The liquid supplement is useful CC for preventing muscle cramps. The method is useful for reducing pollution CC and increasing nutrient availability in an environment or environment or cc environmental sample comprises a soil or a body of water. The immobilized complete by degrading environmental phytic acid, where the environment or cc environmental suseful in foodstuffs for improving the feeding value of CC phytase is useful in foodstuffs for improving the feeding value of cc specification but was created from the wild-type sequence (AEE75418) and cc the information given in claim 1.
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CC The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC endified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase mutant DNA.
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) GRAY K A.
) BARTON N R.
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                                                                                                                            GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400
                     IleValAsnGluAlaArgIleProAlaCysSerLeu
                                                                                                           CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                                                                                                   ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380
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                                         The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as guppy, zebrafish, molly, swordtail, CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase mutant DNA.
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*25-MAY-1999;
25-MAY-2000;
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O' DONOGHUE E.
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al feed; fish feed; dough; ba)
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                                                                                                                                                                                                                                                       GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
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LeuThrProH1sProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                                                                                                                                                                        LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
                                                                                                                                                                                                                                                                                                                               TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
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                                                          ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
                                                                                                             AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
                                                                                                                                                                   GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                                                                                                                                                                                                                                             CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC
                                          CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
                                                                                              GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                                                                                  GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
                                                                                                                                                                                                    AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1997;
01-MAR-1999;
13-APR-1999;
              Formulation useful as dietary supplement for treating, preventing creversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
                                                                                                                                                              Short JI
Baum W,
                                                                                                                                                                                                                                                                             (GARR/)
(ODON/)
(BAUM/)
                                                                                                                                                                                                                                                                                                                                                    (KRET/)
(GRAY/)
(BART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1999;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2004; 2004US-00933115.
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                                                                                                                                                                                                                                                                           SHORT J M.
KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
BAUM W.
                                                                                                                                                                                                                                  ROBERTSON D
ZORNER P.
                                                                                                                                                           , Kretz KA,
Robertson DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA
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2000US-00580515.
2001US-00866379.
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                                                                                                                                                                Gray KA,
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밁 δ S 밁 5 문 S

Disclosure; SEQ ID NO 5; 82pp; English

The present sequence is a DNA sequence related to the production of the CC cover thermostable / protease resistant Escherichia coli phytase CC described in the specification. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity. CC where the polypeptide is a modified sequence (AEB75421) derived from the Escherichia coli K-12 appA phytase (AEB75419). The modification of the CC enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a CC pharmaceutical composition; a kit; an immobilized phytase; a fertilizer or soil additive, a liquid supplement for preventing muscle cramps; a CC hydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising the movel phytase, and a method of reducing CC pollution and increasing the movel phytase, and a method of reducing CC enzyme is a dietary supplement useful for treating, preventing or creversing osteoporosis or bone loss, and preventing muscle cramps. The CC inquid supplement is useful for preventing muscle cramps. The mention or environmental sample by degrading environmental phytic acid, where the environment or environmental sample by degrading environmental phytic caid, where the environment or environmental sample comprises a soil or a body of water. The immobilized phytase is useful in foodstuffs for improving the feeding value of phytate is useful not discussed cramps in the sequence is shown in the sequence listing but not discussed cramps in the specification.

Sequence 1901 ₿₽; 475 A; 499 ü 499 <u>ن</u> 427 Ŧ, 0 U; 1 Other,

Percent Similarity: Best Local Similari Query Match:

Similarity:

Length:
Matches:
Conservative:
Mismatches:
Indels:

Alignment Scores:

No.:

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21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
                                                                                                                 Escherichia coli.
                                                                                                                                         drug design; gene.
                                                                                                                                                     Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                               Prokaryotic essential gene
                                     21-MAR-2002; 2002WO-US009107
                                                                                      WO200277183-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                  CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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Percent Similarity:
Best Local Similarity:
Query Match:

4.8e-195 2182.00 98.1% 98.1% 96.6%

Length: Matches: Conservative: Mismatches: Indels:

Gaps:

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Pred. No.: Alignment

Sequence 1299

BP;

317 A; 345

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355 G;

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US-10-601-319-10 (1-432) x ACA19297 (1-1299)

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ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro

GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180

PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT

120 60

40 60 20

MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla

ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCCGCAATCTGCA

121 41 61 21 _

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid; (2) a host cell containing the vector; (3) an isolated converse of the polypeptide whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway in which a proliferation required gene or required for compound that influences the activity of containing agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling the extent compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for compound that on a culture or collection of strains; or (13) identifying the target of a compound that inhibits proliferation of contains, or for screening homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational containing proteins or screening for homologous nucleic acids required containing proteins or screening homologous nucleic acids required containing proteins and contained acids are useful for containing proteins. The sequence data for this patent did not form part of the printed specification, but was obtained in clettornic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; SEQ ID NO 7167; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or a for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                     ftp.wipo.int/pub/published_pct_sequences
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                                                                                  GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400
                                                                                                                                                                                                                                  PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340
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LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
                                                                                                                                                                              ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380
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Mrachko GT,  Schellenberger
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r V;
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Novel recombinant phytase having modified phytase activity comprising modification of amino acid residues in mature Escherichia coli phytase designated EBC18B2, useful as feed additive.

Claim 19; Fig 21; 107pp; English.

The invention relates to recombinant modified AppA phytases having combified phytase activity. The AppA phytases are derived from a mature Escherichia coli AppA phytases designated EBC18B2 (see ADL16120), and comprise substitutions at least one of residues 26, 43, 46, 54, 73, 113, 2126, 184, 228, 384 or 410, or at a residues 26, 43, 46, 54, 73, 113, 2126, 184, 228, 384 or 410, or at a residue located within 5 residues of those listed above. The invention also encompasses polynucleotides composed a modified AppA phytase and which further encodes a secretion constructs, vectors and host cells (preferably Bacillus subtiliss) comprising the modified AppA phytases. The invention also discloses a method of producing an enzyme having phytase activity; a method of producing a heterologous conjugation and animal feed activity in Bacillus subtilis; reducing the colypeptide having phytase activity; a method of producing a heterologous conjugation animal feed comprising cells, spores or plant parts, compatified AppA phytase; and animal feed comprising cells, spores or plant parts, compatified AppA phytases are useful as an animal feed additive, modified AppA phytases. The modified AppA phytases are useful as an animal feed additive, an important source of phosphorus. The modified AppA phytases also have can be used in the isolation and can phytate enzymes for extracting phosphorus and so have can be used in the isolation and cappalications. For example, they can be used in the isolation and recovery of rare metals to produce lower phosphate homologs of phytate,

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GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACC
                GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                           LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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WPI; 2002-083108/11.
P-PSDB; AAE15807.
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                                                                                                                                                                                                                                                             LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
                                                                                                                                                                                                                                                                                                                                                                CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                              ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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                                                                                                ds; gene; phytate; appA gene; animal feed; inorganic phosphate; enhancement; transgenic; thermal tolerance; protease stability
                                                                                                                                      appA gene encoding phytase
                                                                                                                                                               (first
                                     Location/Qualifiers
                                                                            strain K12
                                                                                                                                                                                                              DNA;
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/product= "Phytase'

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The invention relates to an isolated Escherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids combification from W68E, Q84W, A95P, K97C, S168E, R180Y, N226C or Y277D. CC Also included the E. coli appA gene ADA19449 (or an oligonucleotide containing foodstuff by contacting nutritional value of a phytate-containing foodstuff by contacting the phytase-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in the phytate-containing foodstuff), a method to produce an animal feed containing a microbial phytase (comprising culturing the plant cell, plant part or CC plant under conditions where the nuclectide sequence is expressed and CC converting the plant cells, plants or plants into a composition for animals (comprising the plant seeds, plant CC cells, plant parts or plants in admixture with a phytate-containing codstuff), a method to treat a human or an animal able to benefit from CC comprising administering to the human or animal the plant seeds, plant CC cells, plant parts of a transgenic plant which is modified to centering to the human or animal the plant seed, plant CC cells, plant parts of a transgenic plant which is modified to centering a phytase enzyme, a transgenic non-human organism whose genome CC comprising a heterologous nucleic acid sequence encoding a polypaptide to animal feed and for enhancing digestion in humans and animals. The converted method improves thermal tolerance and protease stability. It calso improves the feeding value of phytate rich ingredients. The present sequence represents the E. coli kil appA gene encoding wild-type phytase.
                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                             Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
                                                                                                                                             Sequence 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 42; Fig 7; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing
                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ADA19450
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US-10-601-319-10 (1-432) x ADA19449

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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
The invention discloses a new isolated or recombinant nucleic acid which encodes a polypeptide having a phytase activity. Also claimed is a nucleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a vector comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, an antisense oligonucleotide, inhibiting the translation of new manage in a cell, a heterodimer comprising the polypeptide and
                                                                                                                       New nucleic acid encoding a polypeptide having in improving the feeding value of phytate rich in phytate digestion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytase; food supplement; enzyme delivery matrix; soybean meal; thermotolerance; thermostability; kernel; phytate; myo-inositol-hexaphosphate; inositol; inorganic phosphate; thermotolerant; feed value; digestion; gene; ds; appA.
                                                                                                   Example
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; 99US-00259214.
99US-00291931.
; 99US-00318528.
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ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC

GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG

GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu

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161

AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis

AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT

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ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGlyLeuIleAlaTyrLeu
                                               GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluIlePheLeuGeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PhelleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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401. .403
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                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                 Alignment
Pred. No.:
                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially csignificant mammals such as guppy, zebrafish, molly, swordtail, cc commercially farmed fish such as guppy, zebrafish, molly, swordtail, cc etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli Kl2 appA phytase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Short .
                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding polypeptide having in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-374952/35.
P-PSDB; ADO50298.
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(BART/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
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                                                                                                                                          MetLysalaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla
                                                                                                                                                                                                                                                                                                                                         1901
ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
                                                                                         TTCGCTCAGAGTGAGCCGGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
                                                                                                        PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
                                     GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
                                                      ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
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; 99US-00259214.
99US-00291931.
; 99US-00318528.
; 2000US-00580515.
; 2001US-00866379.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC

	421 IleValAsmGluAlaArgIleProAlaCysSerLeu 432
420 1447	01 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCys
400 1387	81 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuT
380 1327	61 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuG
360 1267	41 ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArg
340 1207	21 PheIleAlaGlyHisAspThrAsnLew
320 1147	01 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerVa
300 1087	81 ArgThrProGluValAlaArgSerArgAlaThrProLo
280 1027	61 AspSerHisGlnTrpAsnTl 68 GATTCACACCAGTGGAACA
260 967	1 GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTry
240 907	21 LysValSerAlaAspCysValSerLeuThrGi-
220 847	01 LeuLysArgGluLysGlnAspGluSerCysSerLeuThrG
200 787	181 TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
180 727	61 AsnValThrAspAlaIle 68 AACGTGACTGACGCGATC
160 667	41 SerSerProAspProLeu
140	121 AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrYalHisThrGlnAlaAspThr
120 547	01 GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgI
100 487	81 GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLys

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Search completed: June 14, 2006, 10:58:28 Job time : 581.385 secs

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=|abse/ABSSWEB_spool/US10601319/runat_12062006_180103_27735/app_query.fasta_1
-Q=|abse/ABSSWEB_spool/US10601319/runat_12062006_180103_27735/app_query.fasta_1
-DB=Published_Applications_NA_Main -QPMT=fastap_-SUPFIX=rnpbm -MINMATCH=0.1
-LOOPEXT=0 -UNITS=ble -STRAT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs806p
-USER=US10601319 @CCN 1 1 3524 @runat_12062006_180103_27735 -NCPU=6 -ICPU=3
-NORMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                           Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                  Score Match Length DB
   2258 100.0
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA Main:*

1: EMC_Celerra_SIDSJ/ptodata/2/pubpna/US08_PUBCOMB.seq:*

2: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

5: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

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12: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

13: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

14: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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(without alignments)
5637.400 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Sequence 1, Appli
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2 2258 100.0 1308 6 US-10-166-660-1
3 2258 100.0 1308 6 US-10-53-115-9
4 2258 100.0 1308 10 US-10-93-115-9
5 2195 97.2 1301 10 US-10-601-319-6
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24 218.5 96.3 1301 13 US-10-93-115-6
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23 2171 96.1 132 3 US-10-93-115-1
24 218.5 96.5 1381 7 US-11-031-671-4
25 2164 95.8 1486 7 US-10-334-671-4
26 2157 95.5 1281 7 US-10-334-671-4
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29 2169 95.0 1486 7 US-10-284-962-4
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21 2171 96.1 1312 6 US-10-21-733A-1
21 2180 95.0 1486 90.0 US-10-21-733A-1
22 2160 95.0 1486 90.0 US-10-21-733A-1
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24 25.5 1281 7 US-10-21-733A-1
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ALIGNMENTS

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Sequence 1, Application US/11056354

| Sequence 1, Application No. US20050246780A1
| General Information:
| Application No. US20050246780A1
| General Information:
| Applicant: KRETZ, Keith
| Applicant: KRETZ, Keith
| Applicant: Grax, Kevin A.
| Applicant: Grax, Kevin A.
| Applicant: Gray, Nelson R.
| Applicant: Garrett, James B.
| Applicant: O'DONGSHUE, Eileen
| Applicant: O'DONGSHUE, Eileen
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| Applicant: O'DONGSHUE, Eileen
| Applicant: O'DONG
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; PRIOR APPLICATION NUMBER: US 09/291,931; PRIOR FILLING DATE: 1999-04-13; PRIOR APPLICATION NUMBER: US 09/259,214; PRIOR APPLICATION NUMBER: US 08/910,798; PRIOR FILLING DATE: 1999-03-01; PRIOR FILLING DATE: 1997-08-13; NUMBER OF SEQ ID NOS: 4; SOPTWARE: Patentin version 3.1; SEQ ID NO 1; LENGTH: 1296; TYPE: DNA; ORGANISM: Artificial sequence; PEATURE; OTHER INFORMATION: Modified phytase enzymus-11-056-354-1
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AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
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                                                                                             TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                            TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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                                               CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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APPLICANT: MATCHING PRICE TO TITLE OF INVENTION: PHYPASES, NUCLEIC ACIDS ENC. TITLE OF INVENTION: PHYPASES, NUCLEIC ACIDS ENC. TITLE OF INVENTION: AND METHODS FOR MAKING AND FILE REFERENCE: 09010-029007

CURRENT FILE REPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR PILING DATE: 1090-05-25

PRIOR PILING DATE: 1090-05-25

PRIOR PILING DATE: 1999-05-25

PRIOR PILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR TILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FABESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson I
APPLICANT: Garrett, James I
APPLICANT: O'Donoghue, Eil
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Garrett, James B.
O'Donoghue, Eileen
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                                                             GluIlePheLeuGunGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                                                 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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                                       GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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APPLICANT: Garrett, James B.
APPLICANT: Gorrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF ITILE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
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PRIOR PILING DATE: 1997-08-13
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Ro
APPLICANT: Garrett, James B
APPLICANT: O' Donoghue, Eile
APPLICANT: Mathur, Eric J.
                                                                                                               NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Wil
SEQ ID NO 9
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FEATURE:
OTHER INFORMATION: modified phytase
FEATURE:
                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                LENGTH: 1308
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Best Local Similarity:
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LOCATION: (1)...(1296)
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 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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FILE REFERENCE: 564462001822

CURRENT APPLICATION NUMBER: US/10/933,115

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: US/99/866,379

PRIOR PILING DATE: 2001-05-24

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 1999-05-25

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR PILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR PILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOPTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 9
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Alignment Scores:
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Rc
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eile
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APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
TITLE OF INVENTION: THEREOF
                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No. US20040091968A1

GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Gray, Kevin A.

APPLICANT: Barton, Nelson Robert

APPLICANT: Barton, Nelson Robert

APPLICANT: Mathur, Efic J.

TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING

TITLE OF INVENTION: AND USING THEM

FILE REFERENCE: 09010-029011

CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT APPLICATION NUMBER: US/9/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/310,528

PRIOR APPLICATION NUMBER: US 09/310,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/259,214

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PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR PILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

                                                 Percent Similarity:
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                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                    ; FEATURE:
, NAME/KEY: misc feature
; LOCATION: 403 -
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US-10-601-319-6
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TYPE: DNA
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                                       LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gary, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
APPLICANT: Mathur, Eric J.
APPLICANT: Mathur, Eric J.
APPLICANT: Mathur, Eric J.
CURRENT APPLICATION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT PAPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/299,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
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US-10-601-319-5
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TYPE: DNA
ORGANISM: Escherichia
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Sequence 5. Application US/10933115

Publication No. US20050281792A1

GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Gary, Kevith A.

APPLICANT: Garrett, Keith A.

APPLICANT: O Donoghue, Eileen

APPLICANT: O Donoghue, Eileen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 564462001822

CURRENT APPLICATION NUMBER: US/10/933,115

CURRENT APPLICATION NUMBER: US/9/866,379

PRIOR APPLICATION NUMBER: US 99/866,379

PRIOR APPLICATION NUMBER: US 99/866,379

PRIOR APPLICATION NUMBER: US 99/866,379

PRIOR APPLICATION NUMBER: US 99/80,515

PRIOR APPLICATION NUMBER: US 99/318,528

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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: n =
US-10-933-115-5
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                                                 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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IleValAsnGluAlaArgIleProAlaCysSerLeu
                                                                                                                                                                                                                                                                                                       ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp
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                                                                             LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
                                                                                                                                CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                                                                       GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                                                                                                                                                                        CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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TITLE OF INVENTION. Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/23,325
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-16
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US-10-282-122A-7167
; Sequence 7167, Application US/10282122A
; Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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ORGANISM: Escherichia
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Yamamoto, Robert
Forsyth, R.
Xu, H.
                          ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
                                                                                                               TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
  GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
                                                                                                                                             PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
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Malone, Cheryl
Haselbeck, Robert
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Trawick, John
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Zyskind, Judith
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                 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
                                                                              GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                                                                                                CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                                                                                                     ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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Sequence 7, Application US/09866379

PATENT NO. US20020136754A1

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: O'DONOGHUB, Bileen
ITILE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERI370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US 09/515
PRIOR APPLICATION NUMBER: US 09/515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931

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PRIOR APPLICATION NUMBER: US 09/291,931

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PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEO ID NOS: 109

PRIOR FILING DATE: 1999-08-13
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Best Local Similarity:
Query Match:
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NAME/KEY: misc feature
; LOCATION: (1). (1901)
; OTHER INFORMATION: n is any nucleotide
US-09-866-379-7
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US-09-866-379-7
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 1901
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                                                            GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                                                                                         ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC
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RESULT 10
US-09-866-379-9
; Sequence 9, Application US/09866379
; Patent No. US20020136754A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1901)
; OTHER INFORMATION: n is any
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Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 2000-05-25

PRIOR PPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR PILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/292,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR PILING DATE: 1999-08-13

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APPLICANT: GARRETT, James
APPLICANT: O'DONGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
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   SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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KRETZ, Keith
GRAY, Kevin
                                                                        GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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Sequence 3, Application US/10156660

Publication No. US20030103958A1

GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith

APPLICANT: Garrett, Keith

APPLICANT: Garrett, James B.

APPLICANT: O'Donoghue, Eileen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM

FILE REFERENCE: 09010-029007

CURRENT APPLICATION NUMBER: US/10/156,660
                                                                                                                                                                                                                                                                                                                                                                                                                                 IleValAsnGluAlaArgIleProAlaCysSerLeu 432
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PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR PLING DATE: 2001-05-24
PRIOR PLING DATE: 2001-05-25
PRIOR PPLICATION NUMBER: US 09/580,515
PRIOR PPLICATION NUMBER: US 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR PPLICATION NUMBER: US 09/291,931
PRIOR PLING DATE: 1999-04-13
PRIOR PPLICATION NUMBER: US 09/292,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR PPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
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TYPE: DNA
ORGANISM: Escherichia col
FEATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
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GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith A.

APPLICANT: Kretz, Keith A.

APPLICANT: Gray, Kevin A.

APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.

APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.

TITTLE OF INVENTION: RECOMBINANT PHYTASES AND
TITLE OF INVENTION: AND USING THEM
FILE REPERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10601319 Publication No. US20040091968A1
PRIOR APPLICATION NUMBER: US 09/866,379 PRIOR FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 09/580,515
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PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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LOCATION: (188)...(1483)
FEATURE:
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(Sequence 7, Application US/10933115

Publication No. US20050281792A1

(GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith A.

APPLICANT: Garzett, James B.

APPLICANT: Garzett, James B.

APPLICANT: Mathur, Eileen

APPLICANT: Mathur, Eileen

APPLICANT: Molson Robert

APPLICANT: Molson Robert

APPLICANT: Molson Robert

APPLICANT: Mathur, Eileen

APPLICANT: Mathur, Eileen

APPLICANT: Molson Robert

APPLICANT: Molson Bileen

CURRENT O' DONOGHUE, Bileen

APPLICANT: MATHUR, BILEEN

FITLE OF INVENTION: THERBOP

FILE REFERENCE: 564462001822

CURRENT APPLICATION NUMBER: US/10/933,115

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: US/09/866,379

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PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR REILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 7
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ORGANISM: Escherichia col
FEATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
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      CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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APPLICANT: SHORT, Jay M.
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Kevin A.
APPLICANT: BARTON, Nelson R.
APPLICANT: GARRETT, James B.
APPLICANT: O'DONOCHUE, Eileen
APPLICANT: MATHUR, Eric J.
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 564462001803/D1370-9C1
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 19/156,660
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/21,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
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PRIOR APPLICATION NUMBER: US 08
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
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                                        LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240
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APPLICANT: UNTERSACTOR APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eilsen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHY
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US 09/886,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
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PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEG ID NOS: 10
SOFTWARE: Patentin version 3.1
SEG ID NO 5
LENGTH: 1901
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US-09-866-379-5
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     TYPE: DNA
ORGANISM: Escherichia
FEATURE:
                                             LENGTH: 1901
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                                          AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr
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ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300
                                                                                                                  GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                                                                                                    LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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                                                                                                                                                       AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                                                                                                                                                                    CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
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                                                                                                 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1483	IleValAenGluAlaArgIleProAlaCysSerLeu 432	CTGGCAGGATGTGAAGAGCGAAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1447	LeuAlaGlyCysGluGluArgAsnAlaGlyMetCysSerLeuAlaGlyPheThrGln 420	CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGGCCG	GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400	CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1327	ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380	ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGATACTGGTGTTTTGAACGCTGG 1267	ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp 360	TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCGC	PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 1147	LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320	CGCACGCCAGAGGTTGCCCGCAGCCGCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG 1087

Search completed: June 14, 2006, 15:10:36 Job time : 1441.42 secs

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELDEXT=7
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1. /BMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4. /BMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5. /BMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US01_NEW_PUB.seq:*
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Sequence 14217, Application US/10449902

| Publication No. US20060123505A1
| GENERAL INFORMATION: | GENERAL INFORMATION: | APPLICANT: National Institute of Agrobiological Sciences. | APPLICANT: Bio-oriented Technology Research Advancement Institution | APPLICANT: Foundation for Advancement of International Science. | APPLICANT: Foundation for Advancement of International Science. | ITTLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF | FILE REFERENCE: MOA-A0205Y1-US | CURRENT APPLICATION NUMBER: US/10/449,902 | CURRENT APPLICATION NUMBER: US/202-03269 | PRIOR APPLICATION NUMBER: JP 2002-203269 | PRIOR FILING DATE: 2002-05-30 | PRIOR FILING DATE: 2002-12-11 | NUMBER OF SEQ ID NOTE: 2002-12-11 | NUMBER OF SEQ ID NOTE: 2002-13-11 | SOPTWARE: Patentin Ver. 2.1 | SOPTWARE: Patentin Ver. 2.1 | SOPTWARE: Patentin Ver. 2.1
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK064835
DATABASE ENTRY DATE: 2001-12-06
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TYPE: DNA
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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US-10-449-902-9793/c
                                                                                                                                                                                                                                                                                                   Sequence 9793, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: AK107141;
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores: Pred. No.:
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ORGANISM: Oryza sativa
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                                                                                                                                                                                              Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 21879
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072104
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryza sativa
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tGlnAspValThr-ProAspAlaTrpProThrTrpProValLysLeuGly-------
                                                                                                CTTCTCCCGCTCCACGGTCAGCTTCCCTTCCTTGGTGGTGAGCCGGAA-----CAG
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                                                                  SerValVal-IleValSerArgHisGlyValArgAlaProThrLysAlaThrGlnLeuMe 51
                                                                                                                          LeuIleProLeuThrProGlnSerAlaPheAlaGlnSerGluProGluLeuLysLeuGlu 31
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Matches:
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                                           SEQ ID NO 7723
  ORGANISM: Oryza sativa
               LENGTH: 2822
TYPE: DNA
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                                                           GlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrp
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                                                                                                                              GCCGCAGCTAGGAGCGGAGCGGCGGCG-
                                                                                                                                                                                          CysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeu 245
                                                                                                                                                                                                                                                                                                                     GlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAsp
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US-10-449-902-7723/c
Sequence 7723, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-05-31
SEQ ID NOS: 56791

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DATABASE ACCESSION NUMBER: AK105071
DATABASE ENTRY DATE: 2002-08-28
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                                                                              CysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeu
                                                                                                                 GTCGATGCGGCTCCGCAGCTCACGCAGCGAGCACCACCTGCAGGCGGCCGCTGCT
                                                                                                                                             GlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAsp
                                                                                                                                                                                                           ---GluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLys
                                                                                                                                                                                                                                                                                                          GAGGTCGATGTCCTCCGTCTGGATCTCCTGGTTCATGTTGTAGAGCACCTCCACCAGCGC 1758
                                                                                                                                                                                                                                                                                                                                          GinLeuAsp-----AsnAlaAsnValThrAspAlaIleLeuGluArgAlaGlyGlySer 173
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo
US-11-189-279-64
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APPLICANT: LUO, WANG
TITLE OF INVENTION: A METHOD OF TREATING CAN
FILE REFERENCE: UTXC:875US
CURRENT APPLICATION NUMBER: US/11/189,279
CURRENT FILING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: 60/598,554
PRIOR FILING DATE: 2004-08-03
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                                                                    US-10-601-319-10 (1-432) x US-11-284-978-14 (1-1221)
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                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/11284978 Publication No. US20060121508A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: RS0222
CURRENT APPLICATION NUMBER: US/11/284,978
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/633,008
PRIOR FILING DATE: 2004-12-03
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Raymond, Christopher K.
TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORMS OF
TITLE OF INVENTION: PURIMERGIC RECEPTOR P2X, LIGAND-GATED ION CHANNEL,
TITLE OF INVENTION: 3 AND 4 (P2RX3, P2RX4)
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                                                                                                                                                                                                                                                                   LENGTH: 1221
TYPE: DNA
ORGANISM: Homo
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                             TITLE OF INVENTION: Identification of Tumors
FILE REFERENCE: 022041-002020US
CURRENT APPLICATION NUMBER: US/11/145,307A
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 60/577,084
PRIOR FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn version 3.1
SEQ ID NO 189
LENGTH: 2711
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APPLICANT: Erlander, Mark G.
APPLICANT: Ma, Xiao-Jun
ORGANISM: Homo sapiens
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                            AACACGCCACTGGGGGCGCAACCTCTCG-ACTCACCAGACCTACCCCGTGGTGGCAGATCC
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Sequence 1, Application US/10501834

Publication No. US20060088828A1

GENERAL INFORMATION:

APPLICANT: HARTIS, Peter C., Ward, Christopher J., Rossetti, San APPLICANT: Vicente E.

TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids

TITLE OF INVENTION: and Proteins

FILE REFERENCE: 07039/386US1

CURRENT APPLICATION NUMBER: US/10/501,834

CURRENT FILING DATE: 2004-07-19

PRIOR APPLICATION NUMBER: PCT/US03/02038

PRIOR APPLICATION NUMBER: BC0/351,110

PRIOR FILING DATE: 2002-01-23

PRIOR FILING DATE: 2002-01-23

INMBER OF SEQ ID NOS: 221
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TYPE: DNA
ORGANISM: Homo
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                                                                      AGAATGGTGTGGTCTCCCAAAACTCAAAATCACACAAGTAAAAGGACCCGAGAGGTCAACC
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                                -----LeulleAlaTyrLeuGlyHisTyrTrpArgGlnArgLeuValAlaAspGly
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3894 TGCCGCTTCATACATGAAGGTGAAGCCTTTCCCCC------
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                                                                                                                                                                                                                                                                                        uLeuValPheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLe 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACAGTTCAGGTTCCCCAGAAGGATGACTGAGTTGGAGAGGTTACTTCCTCCCACATG 3952
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                                                                                                                                                                                                                                                                                                                                               TTCTGTGGAGACCAGCTGGCAGTGG---GGGCAGTGCCACCTCCAGGCCCCA---AGCCG 3467
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                                                                                                                                                                                                                                      ACTGTGTGTGAACCGGAGCCAAGGCATCCTGGACGTGGACTTCCACATCCAAATCCGTAT 3407
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                   CTGCTATATTGCTTATGTTTCTGCTCAGAGTCACAATAACTGGATTTAAGGAAGAGACAT 330:
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                                                                        ---GluValLysLeuThrLeuAlaGlyCysGluGluArg----
                                                                                                                               - CCTCGCCÁCTCCÁATGACCAGGGTCTCACCGC
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APPLICANT: ROSENDETS, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPHANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT PILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US/10/31,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
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Best Local Similarity:
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SEQ ID NO 358
LENGTH: 3646
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ORGANISM: Homo
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Fry, Kirk
Woodward, Robert
Ly, Ngoc
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ĂTCTCAGGACTCCAGCCTGGCAACTCCTĂCTGGCTGCĂGCTGCGCAGCGAACCTGĂTGGG
                                         IleAlaTyrLeu-----GlyHisTyrTrpArgGln---ArgLeuValAlaAspGly 92
                                                                                                                                                                                                             GCCTCTGCTCTGGACCAGTCTCCATGTGCTCAGCCCACAATGCCCTGGCAAGATGGACCA
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eIleAlaGlyHisAsp----

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AspLysThrProLeuSerLeuAsnThrProProGlyGluVal------
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                                                                        SerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArg
                                      TCAGATACCTGTGAAGAAGTGGAACCCAGCCTCCTT---GAAATCCTCCCCAAGTCCTCA 1770
                                                                                                                     TTTCCTGCACACTACAGGAGACTGAGGCATGCCCTGTGGCCCTCACTTCCAGACCTGCAC 1653
                                                                                                                                                                                                                                                                                      CTCTGCATCTAGTGCTGGGCCTCAGCGCCGTCCTG-GGCCTGCTGCTGAGGTGGCAG
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 315
LEQUID NO 315
FUND. TNAM.
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Best Local Similarity:
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US-11-293-697-315
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ORGANISM: Homo
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618 GCAGGCGCAGGACCC---
                                      124 AlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThrSerSerPro 143
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                                                                                                                       GlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGluAlaPheAla 123
                                                                                                                                                                       ACCAGAAAACGAAGAACGCCCGGAGGCGGGAGGCCAGGCTGC--
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Gaps: S-10-857-260-27 (1-39536) ProLeuThrProGlnSerAlaPheA:	GORGANISM: Felis catus FEATURE: FEATURE: ORGANISM: Felis catus FEATURE: ORGANISM: Felis catus ORGANISM: Felis catus ORGANISM: Felis catus FERATURE: ORGANISM: Felis catus ORG	APPLICANT: Logic A. APPLICANT: Grahn, Robert APPLICANT: Erdman, Carolyn APPLICANT: The Regents of the University of California TITLE OF INVENTION: Carrier Tests for Polycystic Kidney Disease in the Cat FILE REFERENCE: 023070-146800US CURRENT APPLICATION NUMBER: US/10/857,260 CURRENT FILING DATE: 2004-05-28 NUMBER OF SEQ ID NOS: 47 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 27 LENGTH: 39536	52	175 AlaAspPheThrGlyHisTyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPh 783 GGG	Qy 144 AspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAlaAsn 161
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DB:
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Best Local Similarity:
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; ORGANISM: Homo sapiens
US-11-317-329-2
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 2696
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APPLICANT: Inchara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFREENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
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192 LeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSer 211
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                                                   TGGACCCCTCTTCACCTGGCTGCA-----
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                                                                               GlySerIleAlaAspPheThrGlyHisTyrGlnThrAlaPheArgGluLeuGluArgVal 191
                                                                                                                                                                                  CGAGTGGATGAGGATGGCTGGGCCCCACTGCACTTTGCAGCCCCAGAATGGGGATGACCGC 1701
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   Alignment Scores Pred. No.:
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                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2696
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
                                                                                                                                                                                              APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
                                                                                                                                                  PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
                                                                                  TYPE: DNA
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                                                                 Homo
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                                                                 sapiens
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272 HisAsnAlaGlnPheAspLeuLeuGlnArgThrProGluValAlaArgSerArgAlaThr
                                                                                                                                                                                                                                                                                                    ---CCACCTGGCGGTCCAGAGGAGCACCTTCCTGAGTGTCATCAA 2405
                                                                                                                                                                                                                                                                                                                                                              ThrProProGlyGluValLysLeuThrLeuAlaGlyCysGluGlu 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuValPheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeu 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGGAGCTGTGAACTGGACTCC-CCTGCA---CCTAGCTGCACGCCACGGGGAGGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCCACTGCACACTGCCAGCTGCCAGGGGCCAAATACCTGATCTGCAAGATGCTGCTCAGG
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    AGCCAGGGGGCTGAGTTGGATGCTCAGCAGAGAAACCTGAGAACACCACTG

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for Regulating Cellular Signaling
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45 ThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro ::: ::: :::	Oy 26 ProGluLeuLyBLeuGluSerValVallevalSerArgHisGlyValArgAlaPro 44 Oy 26	-10-601-319-10 (1-432) x US-11-317-329-5 (1-2696) 8 PheLeuSerLeuLeuIleProLeuThrProGlnSerAlaPheAlaGlnSerGlu	Alignment Scores: Pred. No.: 8.44 Cength: Score: 96.50 Percent Similarity: 33.1% Best Local Similarity: 21.9% Query Match: 4.3% DB: A.3% Cength: Mismatches: 167 Mismatches: 152 DB: Gaps: 22	328	; NUMBER OF SEQ ID NOS: 44 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 5 ; LENGTH: 2696	CURRENT APPLICATION NUMBER: US/11/317,329 ; CURRENT FILING DATE: 2005-12-22 ; PRIOR APPLICATION NUMBER: US/10/128,174 ; PRIOR FILING DATE: 2002-04-23	APPLICANT: Nunez, Gabriel , APPLICANT: Inohara, Naohiro , APPLICANT: Inohara, Naohiro , TITLE OF INVENTION: MG667 , FILE REPERENCE: IM-0.6967	US-11-317-329-5 US-11-317-329-5 ; Sequence 5, Application US/11317329 ; Publication No. US20060105413A1 ; Publication No. US20060105413A1	QY 392 INTEROPTOGLYGIAVALLYBLEUTINIHEMIAGLYCYBGIAGIA 400	2316 GTGTGGGGCTGACCCCAATGCTGCAGAGCAGTCAGGCTGGACACCCCT	2292GCGTGGTGCACCTGCACCACCTGCACCACCTGCACCACCTGCACCACCTGCACCTGCACCACCTGCACCACCTGCACCACCTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	333 AIALEGGIULEGARRITED III. LEGER COLYGIUE LORI SCHOOL SC	325 2179	313ValThrLeuProThrSerValLeuPheIleAlaGly ::: 2119 TACGGAGCCAGCCTTGAGCTGCCCCACCCACGGCTGGACACCCCTGCATCTAGCAGCC	Qy 312 Gly 312	Db 1999 GCCATCCAACACCTGCTGAAGAGTGGAGCGGTCCCTGATGCCCTTGACCAGAGCGGCTAT 2058

97 CysGlyCysProGlnSerGlyGlnValAlaIleIle	AAGCGGGCCCTTCAGCTCTGGACCGTAAGAATTTGGTCCCGAGAGATGAGGAACTGTGT ALATYLLeuGlyHisTyTTTpArgGlnArgLeuValAlaaspGlyLeuLeuProLys
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-Q=/abss/ABSSWEB spool/US10601319/runat 12062006 180052 27516/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -NINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss03p
-USER=US10601319_@CGN_1 1_12067 - MINLEN=0 -MAXLEN=2000000000 - ICPU=3
-NORME-XTS-0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

	COMMENT	JOURNAL PUBMED	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	Ch662/34
Max-Planck-Institute for Developmental Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72078, Germany Tal: 00497071601371 Fax: 00497071601498 Email: ralf.sommerætuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.	Contact: Sommer RJ	Nucleic Acids Res. 32 (1), D421-D422 (2004) 14681447	AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus	Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.	1 (bases 1 to 853)	Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.	Pristionchus pacificus	Pristionchus pacificus	GSS.	CL662734.1 GI:50150877	CL662734	survey sequence.	pacificus var. California Pristionchus pacificus genomic, genomic	_B11 - PRI0142b.B21 (853) Mixed stage fosmi	CL662734 853 bp DNA linear GSS 09-JUL-2004	

Mochii, M.,

Ueno, N.,

Shin-i,T.

is available through

the following

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Class: fosmid
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BJ074127 NIBB Mochii normalized laevis cDNA clone XL090j06 5', m
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Xenopus laevis (African clawed Xenopus laevis
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/clone_lib="Mixed stage
var. California"
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/mol_type="genomic DNA"
/strain="California"
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249 GlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsnThrLeu 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 616)
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                                                                                                AGCTGTTCATTAACGCAGGCATTACCATCGGAACTCAAGGTGAGCGCCGACAATGTCTCA
                                                                                                                  SerCygSerLeuThrGlnAlaLeuProSerGluLeuLygValSerAlaAspCysValSer
                                                                                                                                                              GAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAA
                                                                                                                                                                                                                               AGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCATCGGCAAACGGCGTTTCGCGAACTG
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/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:8355"
/clone="XL090j06"
/tlssue_type="whole embryo"
/clone_lb="NtDB Mochii normalized Xenopus tailbud
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

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SJAABUGG2 Adult SjC 7/94 Schietosoma japonicum cDNA similar to
pdb|1DKP|A Chain A, Crystal Structure Of Phytate Complex Of
Escherichia Coli Phytase At Ph 6.6. Phytate Is Bound With Its
3-Phosphate In The Active Site. Hg2+ Cation Acts As An
Intermolecular Bridge, mRNA sequence.
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351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922.
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/ BEAR MADIE DOOD,
// tissue type="whole body"
// lab_host="Mouse and rabbit"
// lab_host="Mouse and rabbit"
// clone lib="Adult SjC 7/94"
// clone lib="Adu
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Location/Qualifiers
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/mol type="mRNA"
/strāin="Chinese (Anhui) strain"
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clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

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RESULT 4
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Vettore, A.L., da Silva, F.R., Kemper, B. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                  Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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Query Match:
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  344
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Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br plate: 001 row: D column: 10 Seg primer: M13/Porward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: parruda@unicamp.br
                                                              GlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuPro 343
                                                                                                                                         HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla
                                                                                                                                                                                                                                                                                               GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSer
GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu 363
                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT
                                                                                                                                                                                                                                                                                                                                                                             LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis
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                                                                                                                 CATCCACCGCANAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCC
                                                                                                                                                                                             GAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC
                                                                                                                                                                                                                                                                        /clone lib="CL2"
/clone lib="CL2"
/clone lib="CL2"
/note="Organ: Pool of sugarcane calli submitted to low
/note="Organ: Pool of sugarcane calli submitted to low
(4oC) and high (37 C) temperature stress; Vector:
pBlurScript; Site 1: EcoRI; Site 2: XhoI; An
unidirectional cDNA library generated from [Pool of
sugarcane calli submitted to low (4oC) and high (37 C)
temperature stress]. cDNA was prepared from polyA+ mRNA
using ZAP - cDNA Synthesis Kit (Stratagene). The
double-strand cDNAs were fractionated in a sepharose CL-2B
40cm-columns and fragments sizing between 0.8 and 1.5 Kb
were directionally cloned into the vector. Details of
each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'mol_type="mRNA"
'db_xref="taxon:4547"
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888.00
96.7%
96.7%
39.3%
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Alignment
Pred. No.:
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CF326092/c
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                                                                                                                                                      US-10-601-319-10 (1-432) x CF326092 (1-595)
                                                                                                                                                                                                                Query Match:
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Best Local Similarity:
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JOURNAL
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                                                                                                                                                                                                                                                                                           . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FION JMT1--05-B09.g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA clone JMT1--05-B09, mRNA sequence.
CF326092
CF326092.1 GI:33800445
SEST.
Oryza sativa (japonica cultivar-group)
ISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enthartoideae; Oryzeae; Oryza.

1 (bases 1 to 595)
                                                                                                                                                                                                                                                                                                                 Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 595)
1 (bases 1 to 595)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, (
of Bioscience and Bioinformatics,
Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, K
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
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GCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAG
                    AlaThrProLeuLeuAspLeuIleLysThrAlaLeuThrProHisProProGlnLysGln
                                                                           AGTITIGCATAACGCGCAATTITATTTGCTACAACGCACGCCAGAGGTTGCCCCGCAGCCGC 536
                                                                                                   SerLeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrProGluValAlaArgSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Nackdong"
/db xref="taxon:39947"
/clone="JMT1--05-B09"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="14 days after germination"
/lab_host="L.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JWT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/NoI; cDNA was inserted into lamda Uni-ZAP XR vector at
end with EcoRI and 3' end with XhOI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Oryza sativa (japonica cultivar-group)"
|mol_type="mRNA"
                                                                                                                                                                                                              2.93e-75
847.00
99.4%
99.4%
37.5%
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Matches:
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, MyongJi University
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CN762997/c
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                                                                                                                                                                                                    UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
FOR PRIMERS
FORWARD: CAGGARACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                        Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Acyrthosiphon pisum
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta;
Reoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 895)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Mu
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CN762997
CN762997.1 GI:47536920
EST.
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ID0AAA5DC09RM1
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                                                                                                                                                                                                                                                                                                                                       INRA Rennes
                                                                                                                                                                                                                                                                                                                                                    Contact: D.
                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                              expressed sequence tags database for
                                                                                                                                                                                         ຫ
                                                                                                                                                                         CAGGAAACAGCTATGACC row: C column: 9. Location/Qualifiers
                                           /clone="IDOAAA5DC09"
/tlssue type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic
/lab_host="XII-Blue"
                                                                                                   /organism="Acyrthosiphon pisum"
|mol_type="mRNA"
/cultivar="devolopmentstage"
|db_xref="taxon:7029"
               /clone_lib="ApMS"
/note="Vector: pB:
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"Vector: pBS-SK minus; Site 1: EcoRI; Site_2: XhoI; name: IDOAAA; Plant growth place: Department of
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Acyrthosiphon
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cDNA clone
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IDOAAASDC09 5',
                                                         females)"
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Ecology & Evolutionary Biology, Princeton University; soil conditions: Soil; Sowing date: 01/66/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

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SOURCE
ORGANISM
                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                               RESULT 7
CN754382/c
LOCUS
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Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidifa
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

(bases 1 to 868)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyr
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Aphidiformes;
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Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
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Plate: 12 row: E column: 1.
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                                                                                 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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/lab_host="XL1-Blue"
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/mol_type="mRNA"
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 864)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiph
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Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchhera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
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Contact: D. Tagu
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Acyrthosiphon pisum
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ThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAlaLeu 301
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                                                                                                                                                                                                                                                                                                           /note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: IDOAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c) "
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lab_host="Xil-Blue"
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'cultivar="developmentstage"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 383)

Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,

Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B.,

Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C.,

Martin, G.B., Tanksley, S.D. and Giovannoni, J.

Generation of EGTs from tomato seed tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW036132
383 bp mRNA linear EST 18-MAY-2001 EST274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.
AW036132
AW036132.1 GI:5894811
                                                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                             Contact: CUGI
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                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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                                                                                                                                                                                                                                                  sequence.
         /dev stages "quiescent seed"
//lab_host="XL1-Blue MRF'"
//lab_host="XL1-Blue MRF'"
//lab_host="XL1-Blue MRF'"
//lab_host="XL1-Blue Script SK(-); Site 1: EcoR1; Site
//note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site
Xhol; CLEE - Tomato Seed EST Library. Directionally cl
Xhol; CLEE - Tomato Seed EST Library. Directionally cl
CDNAs inserted into pBlueScript SK(-) at 5' end with
ECORI and 3' end with XhoI site."
                                                                                                                                     /cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEE1823"
                                                                                                                                                                                  organism="Lycopersicon/mol_type="mRNA"
                                                                                                                     tissue_type="seeds"
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Contact: CUGI
                                                                                                      prime
                                                                                                      sequence.
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US-10-601-319-10 (1-432) x AW036132
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                        SerMetLeuThrGluIlePhe 243
                                                                                                                                         TCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTA
                                                                                                                                                                   SerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeu
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TCAATGCTGACGGAGATATTT
                                                                       CCATCGGAACTCAAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCA
                                                                                            ProSerGluLeuLysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAla
                                                                                                                                                                                                                TTTACCGGGCATCGGCAAACGGCGTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAA
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AW036134

AW036134

EST274510 tomato seed, TAMU Lycopersicon esculentum cDNA clone cLEEREZ3 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

RSION

RSION

AW036134

AW036134

AW036134. GI:5894813

EYCOPERSICON esculentum (Solanum lycopersicum)

Lycopersicon esculentum material phosphyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Indidg, Solanales; Solanaceae; Solanum; Lycopersicon.

FERENCE 1 (bases 1 to 383)

AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tankeley, S.D. and Glovannoni, J.

Generation of EST's from tomato seed tissue

MMENT Clemson University Genomics Institute

Clemson University Genomics Institute

Clemson University Genome.clemson.edu/orders/index.html

S prime sequence.

// Location/Qualifiers
// Location/Qualifiers
// Cultivar="TA496"
// Lone="CLEERI23"
// Lisue type="seeds"
// Lisue type="seeds"
// Lisue type="seeds"

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                          393 bp mRN M11B12STM Arabidopsis developing seed clone M11B12 5', mRNA sequence.
                                 Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University,
                                                                                                                                          1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogsel. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeu
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//lab_host="XL1-Blue MRP"."
//clone lib="tomato seed, "TANU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
/note="Vector: pBlueScript SK(-); Directionally cloned xho1; CLEB - Tomato Seed EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
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Arabidopsis thaliana cDNA
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BST.
Schistosoma japonicum
Schistosoma japonicum
Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Di
Prideidida; Schistosomatoidea; Schistosomatidae;
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Email: benning@nsu.edu

Michigan State University DNA Sequencing Facility Arabidopsis

Biological Resource Center, The Ohio State University, 309 Bot

Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                         BU713769 531 bp mRNA linear EST 23-OCT-200 SJAABUG01 Adult SjC 7/94 Schistosoma japonicum cDNA similar to sp|P07102|PPA_ECOLI PERIPLASMIC APPA PROTEIN PRECURSOR [INCLUDES:
                                                                                                             BU713769.1
                                                                                                                               BU713769
                                                                                                                                                  SP P07102 PPA ECULI FERTE PROSPHOHYDROLASE
                                                                                                                                            6-PHYTASE ], mRNA sequence.
                                                                                                                                                                                                                                                                                            ValSerLeuThrGlyAlaValSerLeuAlaSer 237
                                                                                                                                                                                                                                                                                                                                 AspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspCys 226
                                                                                                                                                                                                                                                                                                                                                                                                                  GluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: p'
Site_1: EcoRI; Site_2: XhoII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="seed"
/dev_stage="5-13 days
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3702"
/clone="M11B12"
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e; Schistosoma.
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 531)
Hu,W. Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
Xu,X.N., Wang,S.Y., Chen,Z. and Han,Z.G.
Bvolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                      AlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe
                             LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 263
                                                                                                         GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ucv_bruges Adult worms

/lab host="Mouse and rabbit"
/clone_lib="Adult $jC 7/94"
/clone_lib="Adult $jC 7/94"
/clone_lib="Adult $jC 7/94"
/clone_lib="Adult $jC 7/94"
/note="Vector: Lambda ZaP-II XR.; Site_l: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbana, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oilgo dT
chromatography, using a kit from pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oilgo-dT-XhoI-primer and synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
clones contain inserts that appear to be highly homologous
to sequences from salmonoid fishes, as determined by
homology commarisons using BLAST and by Southern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Schistosoma japonicum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="Whole body"
/dev_stage="Adult worms"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:6182"
/sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Chinese (Anhui) strain"
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Conservative:
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SOURCE
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CN759004/c
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                                                                                                                                                                                                                                                                                                                                                                                                               UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P. An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Acyrthosiphon pisum
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 706)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: D. Tagu
INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
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/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: IDOAAA; Plant growth place: Department of
                                                                                  /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                            db_xref="taxon:7029"
clone="IDOAAA24BC04"
                                                                                                                                                                                                           mol_type="mRNA"
cultivar="developmentstage"
                                                                                                                                                                                                                                                              organism="Acyrthosiphon pisum"
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AUTHORS
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AA545747/c
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DB:
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Best Local Similarity:
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WashU-MGB/NHGRI EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                          National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda,
                                                                                                                                                                                                                                 Medical Genetics Branch
                                                                                                                                                                                                                                                       Contact: Libin Jia
                                                                                                                                                                                                                                                                           Unpublished (1997)
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1 (bases 1 to 354)
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                                                                                 il: libin@helix.nih.gov
primer: M13 Reverse.
    Location/Qualifiers
                                                                                                                                                301-402-4877
301-496-7157
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Stromal Fibroblast Homo sapiens cDNA
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RESULT 15
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                                                 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tbhin@genes.nig.ac.jp The information of this clone is availal
                                                                                                                                                             Contact: Tadasu Shin-i
Center For Genetic Res
                                                                                                                                                                                                                                              Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
1 (Dases 1 to 707)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N
                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                          BJ619443.1 GI:37258203
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                            BJ619443

707 bp mRNA linear EST 01-OCT-BJ619443 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL189d24 5', mRNA sequence.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                              Unpublished (2001)
                                                                                                                                                                                                                Expressed genes in X. laevis
                                                                                                                                                                                                                                   Kohara,Y
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/cell_type="stroma! fibroblast"
/dev stage="mixed"
/lab_host="XL1-Blue"
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/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI"
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108
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source	CO E	707			
ORIGIN		"mol_type="mRNA" (db_rref="taxon:8355" (clone="XL189d24" 'tissue_type="whole embryo" (dev_stage="stage 10.5" (clone_lb="NIBB Mochii normalized	355" le embryo" 10.5" dochii normalize	d Xenopus early gastrula	1a
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\$	251 MetProG	luProGlyTrpGlyArgI	[leThrAspSerHisG	MetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsnThrLeuLeuSer 2	270
₽	2 ATGCCGG	AGCCGGGGTGGGGAAGGA	ATCACCGATTCACACC	TGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAACACCTTGCTAAGT 61	1
ş	271 LeuHigA	mAlaGlnPheAspLeuL	euGlnArgThrProG	LeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrProGluValAlaArgSerArgAla 2:	290
망	62 TTGCATA	CGCGCAATTTTATTTGC	TACAACGCACGCCAG	TTGCATAACGCGCAATTTTATTTGCTACAACGCACGCCAGAGGTTGCCCGCAGCCCGCCC	21
Ş	291 ThrProLe	uLeuAspLeuIleLysT	hrAlaLeuThrProH	ThrProLeuLeuAspLeuIleLysThrAlaLeuThrProHisProProGlnLysGlnAla 310	10
В	122 ACCCCGTT	ATTAGATTTGATCAAGA	CAGCGTTGACGCCCC	ACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAACAGGCG 181	31
δ	311 TyrGlyva	lThrLeuProThrSerV	/alleuPheIleAlaG	TyrGlyValThrLeuProThrSerValLeuPheIleAlaGlyHisAspThrAsnLeuAla 330	ő
망	182 TATGGTGT	GACATTACCCACTTCAG	TGCTGTTTATCGCCG	TATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGCA 241	11
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Q3z3el shiqella so
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Q7afw3 escherichia
Q7w109 escherichia
Q8w29 escherichia
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Q8y22 citrobacter
Q6u677 citrobacter
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osphoanhydride obhatase) (AP); 4- interobacteriales; interobacteriales; interobacteriales; chia coli gene appA l phosphatase and l c., Mayhew G.F., M.A., Rose D.J., i K-12."; i K-12."; i K-12."; i K-12."; i K-12."; i K-12."; i K-12."; i K-12."; i R-12."; i I region of the ph 2.5 li region of the ph 2.5 li region of the ph 2.5 li region of the ph 2.5		0827pl salmonella Q52309 providencia Q6ev19 enterobacte Q9aaq4 caulobacter Q8pp76 xanthomonas Q4ur06 xanthomonas Q1bxb8 xanthomonas Q1bxb8 xanthomonas Q5px75 xanthomonas Q5gx75 xanthomonas Q6cxf4 erwinia car Q8pf53 xanthomonas Q6gxf3 xanthomonas Q8pf37 xanthomonas Q8pf37 xanthomonas Q8pf37 xanthomonas Q8pf37 xanthomonas

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STRAIN=K12;
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FSihi H.,
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Nat. Struc
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NUCLEOTIDE
EMBL;
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MEDLINE=93256556; PubMed=8387749; DOI=10.1006/abbi.1993.1261;
Greiner R., Konietzny U., Jany K.-D.;
"Purification and characterization of two phytases from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greiner R., Jany K.-D.; "Characterization of a phytase from Escherichia coli."; Biol. Chem. Hoppe-Seyler 372:664-665(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A new oxygen-regulated operon in Escherichia coli
for a putative third cytochrome oxidase and for pH
phosphatase (appA).";
mol. Gen. Genet. 229:341-352(1991).
                                                                                                                  Copyrighted
Distributed
                                                                                                                                                                                                                                                                                                         "Overexpression, site-directed mutagenesis, Escherichia coli acid phosphatase."; J. Biol. Chem. 267:22830-22836(1992).
                                                                                                                                                                                                                                                                                                                                           MEDLINE=93054596; PubMed=1429631; Ostanin K., Harms E.H., Stevis P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli."
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               IBL; M58708; AAA72086.1; -; Genomic_DNA.
IBL; U00096; AAC74065.1; -; Genomic_DNA.
IBL; D90735; BAA35745.1; -; Genomic_DNA.
IBL; X05471; CAA29031.1; -; Genomic_DNA.
IBL; X05471; CAA29031.1; -; Genomic_DNA.
IBL; M58708; -; NOT_ANNOTATED_CDS; Genomic_DNA.
IBL; M58708; -; NOT_ANNOTATED_CDS; Genomic_DNA.
IBL; S63811; AAB22286.1; -; Genomic_DNA.
IR; B36733; B36733.
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IDKN; X-ray; AB23-432.
IDKN; X-ray; AB23-432.
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                                                                                                                                                                                                               phosphate.

CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)0 = 1D-
                                                                                                                                                                                                                                 Struct. Biol. 7:108-113(2000).
CATALYTIC ACTIVITY: A phosphate monoester +
                                                                                                                                                                                                                                                                                                                                  Etten R.L.;
                                                                                                                                            aerobic to anaerobic conditions.
SIMILARITY: Belongs to the histidine acid phosphatase family.
                                                                                                                                                    SUBCELLULAR LOCATION: Periplasmic.

INDUCTION: In addition to CAMP-mediated control, this enzy induced when bacterial cultures reach stationary phase; it synthesis is triggered by phosphate starvation or a shift serobic to anaerobic conditions.
                                                                                                                                                                                                 myo-inositol 1,2,3,4,5-pentakisphosphate SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. 303:107-113(1993).
                                                                                                                                                                                                                                                                      Golovan S.,
                                                                                                                                                                                                                                                             Structures of Escherichia coli phytase and i
X-ray;
X-ray;
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                                                                                                                  under the Creative Commons Attribution-NoDerivs License
                                                                                                                           by the UniProt Consortium, see http://www.uniprot.org/terms
; A/B=23-432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1658595; DOI=10.1007/BF00267454; ., Marck C., Dion M., Kieffer-Bontemps M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE
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pH 2.5 acid
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 Genema:
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EchoBASE; EBUU*,
EchoBASE; EBUU*,
EchoBASE; EBUU*,

R EchoBASE; EGI0049; appA.

R InterPro; IPR000560; HisAc_phsphtse.
R Ffam; pF00328; Acid phosphat A; 1.

JR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.

DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

OR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
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EL -> DV (in Ref. 4).
D -> S (in Ref. 4).
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Nucleophile.
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PubMed=16275786; DOI=10.1093/nar/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y.,

Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun

Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z

Qiang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species, the

agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).
 EMBL; CP000038; AAZ87721.1; -; Genomic DNA. GO; GO:003993; F:acid phosphatase activity; InterPro; IPR000560; HisAc phosphate. Pfam; PF00328; Acid phosphat A; 1. PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1. PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN PROSITE; PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; HISA_CID_PHOSPHAT_2; UNKNOWN PS00778; UNKNOWN PS00778; UNKNOWN PS00778; UNKNOWN PS00778; UNKNOWN PS00778; UNKNO
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EMBL; AP537219; AAN28334.1; -; Genomic_DNA.
HSSP; P071012; 1DKM.
SMR; OBGN88; 23-432.
GO; GO:0003993; F:acid phosphatase activity;
InterPro; IPR000560; HisAc_phashtse.
Pfam; PPF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOW.
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01-MAR-2003,
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Chen Y., Zhu Z., Zhang Z., He J.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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Name=appA;
Escherichia coli.
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Ostanin K., Harms
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Dassa J., Marck C., Boquet P.L.;
"The complete nucleotide sequence of reveals significant homology between
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                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                             "Overexpression, site-directed mutagenesis, Escherichia coli acid phosphatase."; J. Biol. Chem. 267:22830-22836(1992).
      EMBL;
                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                              PubMed=1429631;
E.H., Stevis P.E.,
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      -; Genomic_DNA.
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Pred. No. 1.9e-161;
1; Mismatches 8;
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RESULT 5
QBRKD7, ECOLI
ID QBRKD7, E
AC QBRKD7, E
AC QBRKD7, E
DT 01-JUN--
DT 07-FEB--
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SMR; QBRXD6; 23-432.

GO; GO:0003993; F:acid phosphatase activity; IE
GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR000560; HisAc_phsphtse.
Pfam; P070328; Acid_phosphat A; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT 1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN_Hydrolase.
                                                                                         NUCLEOTIDE SEQUENCE.

MEDLINE=90368616; PubMed=2168385;

MEDLINE=90368616; PubMed=2168385;

DABBA J., MARCK C., Boquet P.L.;

"The complete nucleotide sequence of the complete nucleotide sequence of the reveals significant homology between placese-1-phosphatase.";

J. Bacteriol. 172:5497-5500(1990).
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                                                                                                                                                                                                                                                                                                                                                    Name=appA;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002, integrated into U
01-JUN-2002, sequence version
07-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                               Periplasmic
    MEDLINB=93054596;
Ostanin K., Harms
                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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PubMed=1429631;
E.H., Stevis P.E.,
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Pred. No. 2.
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pH 2.5 acid phosphatase
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RESULT 6
QBRKDB_ECOLI PRELIMINARY; PR
ID QBRKDB;
AC QBRKDB;
DT 01-JUN-2002, integrated into Unit
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Periplasmic phosphoanhydride pho
GN Name-appA;
OS Escherichia coli.
OC Bacteria, Proteobacteria; Gammap:
OC Enterobacteriaceae; Bscherichia.
OX NCBI TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RY MEDLINE=90368616; PubMed=2168385
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GO; GO:0003993; F:acid phosphatase activity; GO; GO:0015787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc phsphtse.
Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNO Hydrolase.
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NUCLEOTIDE SEQUENCE.
MEDLINE=90368616; PubMed=2168385;
                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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li acid phosphatase.";
267:22830-22836(1992).
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Periplasmic

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QBRKEO;
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01-JUN-2002, sequence version 1
07-FEB-2006, entry version 13.

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SEQUENCE
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GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; Hisac phsphtse.
Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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J. Bacteriol. 172:5497-5500(1990).
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B.H., Stevis P.B.,
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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SMR; QBRKE0; 23-432.

GO: GO:0003993; F:acid phosphatase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR000560; HisAc_phsphtse.

Pfam; PF00328; Acid_phosphat_A; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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Chem. 267:22830-22836(1992).
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Pred. No. 2.7e-161;
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01-JUN-2002, integrated into Uni
1 01-JUN-2002, sequence version 13.
7 07-FEB-2006, entry version 13.
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GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid_phosphat_A; 1.
PROSTIE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_
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"The complete nucleotide sequence of reveals significant homology between glucose-1-phosphatase.";
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Enterobacteriaceae; Escher
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Escherichia coli.
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MEDLINE=90368616; PubMed=2168385;

Dassa J., Marck C., Boquet P.L.;

"The complete nucleotide sequence of the reveals significant homology between pt glucose-1-phosphatase.";

J. Bacteriol. 172:5497-5500(1990).
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HSSP; P07102; 1DKM.
SMR; QBRKD5; 23-432.
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van Etten R.L.;
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MEDLINE=93054596; Po
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Enterobacteriaceae; Escherichia.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CP000036; ABB66815.1; -; Genomic DNA.
GO; GO:0003993; F:acid phosphatase activity; IEA.
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Name-apph; OrderedLocusNames-SBO_2250;
Shigella boydii serotype 4 (strain Sb227).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agents of bacillary dysentery.";
Nucleic Acids Res. 33:6445-6458(2005).
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PubMed=16275786; DOI=10.1093/nar/gk1954;
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LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                     BIFLLQQAQGMPBPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
                                                                                                                  ROTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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                                                                BIFLLQQAQGMPBPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
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Pred. No. 1.4e-159;
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X., Sun L., Chen S.,
Y., Yao Z., Shen Y.,
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Phosphoanhydride p
Name=appA; Ordered
Shigella flexneri.
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GO; GO:000393; F:acid phosphatease activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid phosphat A; 2.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
COMPACTOR STATES
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE005674; AAN42610.2; -; Genomic_DNA. SMR; Q83RW2; 23-432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
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RESULT 12
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DE Acid phosphates
GN Name=appA2;
OS Escherichia cc
OC Enterobacteria;
OX NCBI_TaxID=562
RN [1]
RP NUCLEOTIDE SEC
RN [1]
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RN [2]
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RA Lei X.G.;
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Pfam; PF00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT 1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.
CHAIN
20
432
A32
A47042 MW; 71B0E5EEDZEA2674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, sequencing, and expression of an Escherichia coli
phosphatase/phytase gene (appA2) isolated from pig colon.";
Biochem. Biophys. Res. Commun. 257:117-123(1999).
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MEDLINE=99194564; PubMed=10092520; DOI=10.1006/bbrc.1999.0361;
Rodriguez E., Han Y., Lei X.G.;
Rodriguez E., Lei X., Lei
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05-JUL-2004, sequence version
07-FBB-2006, entry version 8.
Acid phosphatase/phytase 2.
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GO; GO:0003993; F:acid phosphatase activity;
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Lei X.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY496073; AAR87658.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
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ROTAFRELERVLNFSQLNLCLNREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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96.8%;
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Pred. No. 5.1e-159;
0; Mismatches 14;
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Best Local Similarity
Matches 417; Conserv
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STRAIN=2457T / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

DOI=10.1128/JAI.71.5.2775-2786.2003;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";

Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                             GenomeReviews; AE014073 GR; S1048.
GO; GO:000393; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc_phsphtee.
Pfam; PF00328; Acid_phosphat A; 1.
PROSITE; PS00718; HIS ACID_PHOSPHAT 1; UNKNOWN 1.
PROSITE; PS00778; HIS ACID_PHOSPHAT 2; UNKNOWN 1.
SEQUENCE 432 AA; 47136 MW; 200442239BC66DFC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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96.5%;
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200442239BC66DFC CRC64;
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RESULT 14

Q7AFW3_ECOS7
ID Q7AFW3;
AC Q7AFW3;
DT Q5-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 10.
DT 07-FBB-2006, entry version 10.
DT 07-FBB-2006, entry version 10.
DE Phosphoanhydride phosphorylase.
QN CPGB-72006, entry version 10.
DE Phosphoanhydride phosphorylase.
QN CPG-72006, entry version 10.
DE Phosphoanhydride phosphorylase.
QN CPG-72006, entry version 10.
DE Bacteria; Proteobacteria; Gammaproteobacteria; Ent CPG-72006, entry version 10.
DE Bacteria; Proteobacteria; Gammaproteobacteria; Ent CPG-72006, entry version 10.
DE CRITICE SEQUENCE [LARGE SCALE GENOMIC DNA].
RN NUCLEOTIDE SEQUENCE A34 AA; 47337 MW; F197DF7D1869F9C4 CR
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Best Local Similarity
Matches 419; Conserv
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STRAIN-0157:H7 / Sakai / RIMD 0509952 / EHEC;
MEDLINE-21156231; PubMed-11258796; DOI=10.1093/dnares/8.1.11;
MEDLINE-21156231; PubMed-11258796; DOI=10.1093/dnares/8.1.11;
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"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc phsphtse.
Pfam; PF00328; Acid phosphat A; I.
PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1.
SEQUENCE 434 AA; 47337 MW; F197DF7D1869F9C4 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
119 GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFT
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                                                                                                                                                                                                                                                                         Score 2144; DB 2; Length 434;
Pred. No. 8.7e-159;
D; Mismatches 13; Indels
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RGO; GO:0003993; F:acid phosphatase activity; IEA.

IR InterPro; IPR000566; HisAc phosphate.

R Pfam; PF00328; Acid phosphat A; 1.

R PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.

R PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1.

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Matches
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PIR; H90770; H90770.
HSSP; P07102; 1DKL.
SMR; Q8XC29; 35-444.
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STRAIN-0157:H7 / EDL933 / ATCC 700927 / EBC5.

MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

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Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

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Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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29 ECO57
PRELIMINARY; PRT; 444 AA.
Q8XC29 ECO57
Q8XC29;
Q1-MAR-2002, integrated into UniProtKB/TrEMBL.
Q1-MAR-2004, sequence version 2.
Q5-JUL-2004, sequence version 17.
Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase; periplasr Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase; periplasr Name=appA; OrderedLocusNames=z1397;
Bscherichia coli Q157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE005174; AAG55528.1; -; Genomic_DNA.
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NCBI_TaxID=83334;
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                                                                                                                                95.0%;
llarity 96.5%;
Conservative
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                                                                                                                         Score 2144; DB 2;
Pred. No. 9e-159;
0; Mismatches 13;
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                                                                     RWRRLSDNSQWIQVSLVFQTLQQWRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGF
                                                                                                            IALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFE
                                                                                                                          TALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFE
                                                                                                                                                                   LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM
                                                                                                                                                                                   LTEIFILQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIK
                                                                                                                                                                                                                          GHRQTAPRELERVLNFPQSNLCLNREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM
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Search completed: June 13, 2006, Job time: 190.248 secs 10:28:33

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Result
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-MODEL-strame+ p2n.model -DEV=xlp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                     Score
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seq length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

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9: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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US-09-866-379-9

US-09-866-379-6

US-09-866-379-6

US-09-259-214-1

US-09-291-931-1

US-09-291-931-1
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ALIGNMENTS

US-09-866-379-7 J. Sequence 7, Application US/09866379 Patent No. 6855365

APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin

RESULT 1

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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILLING DATE: 2000-05-25
PRIOR PILLING DATE: 1909-05-25
PRIOR PILLING DATE: 1999-05-25
PRIOR PILLING DATE: 1999-04-13
PRIOR PILLING DATE: 1999-04-13
PRIOR PILLING DATE: 1999-03-01
PRIOR PILLING DATE: 1999-03-01
PRIOR PILLING DATE: 1999-03-01
PRIOR PILLING DATE: 1999-03-01
PRIOR PILLING DATE: 1999-03-01
PRIOR PILLING DATE: 1997-08-13
                                                                                SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                   NUMBER OF SEQ ID NOS: 10
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                        PatentIn version 3.1
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Pred. No.:
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                                                                                                                                 LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240
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                                        AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln 280
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                                                          ; ORGANISM: Escherichia coli
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1901)
; OTHER INFORMATION: n is any
US-09-866-379-9
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  Percent Similarity:
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Pred. No.:
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GENERAL INFORMATION:
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
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APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUS, Elleen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/518,528
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 1901
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Sequence 5, Application US/09866379

Sequence 5, Application US/09866379

Patent No. 6855365

GENERAL INFORMATION

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: GRAY, Kevin

APPLICANT: BARTON, Nelson

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: DIVER1370-7

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEO ID NOS: 10
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Query Match:
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                                                                ArgArgLeuSerAspAsnSerGinTrpIleGlnValSerLeuValPheGlnThrLeuGln 380
                                                                                                                                         ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp
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GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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APPLICANT: GARTIN, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOCHUE, Eileen
ITITE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/292,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: (1)..(1901) OTHER INFORMATION: n in
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TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
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                                                                                                                                   TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
                                                                                                                                                       PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
                                                                                                                                                                                                                                  MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla 20
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                                                   GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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                                                                                                            CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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LENGTH: 1323

TYPE DA

ORGANISM: Escherichia co
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc_feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A
US-09-259-214-1
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APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVERL370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
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GENERAL INFORMATION:
APPLICANT: Kretz, Keith
IITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,798
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
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US-09-318-528-1
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Sequence 1, Application US/09291931A
PATCHI NO. 6190897
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
FILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER RPILICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
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                                                                                                                                                                                  TYPE: DNA
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc_feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                     TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCCACTTCAGTACTG
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Best Local Similarity:
Query Match:
DB:
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SEQ ID NO 1

LENGTH: 1323

TYPE: DNA

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1320)

NAME/KEY: misc_feature

LOCATION: (1)...(1323)

OTHER INFORMATION: n = A,T,C
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TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/02903
CURRENT APPLICATION NUMBER: US/09/580,515
CURRENT FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR PELLY DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-04-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR TILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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Patent No. 67200
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GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                                ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGluLeuIleAlaTyrLeu
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GENERAL INFORMATION

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: KRETZ, Kelth

APPLICANT: KRETZ, Kelth

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: O'DONOGHUE, Eileen

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

PILE REFERENCE: DIVERL370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

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ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1323)
OTHER INFORMATION: n is any nucleotide
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GENERAL INFORMATION:
APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OP INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/09/715,477
                                                                                                          Sequence 2, Application Patent No. 6841370
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; ORGANISM: Escherichia
US-09-715-477-2
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Best Local Similarity:
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SEQ ID NO 2
LENGTH: 1486
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PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
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GENERAL INFORMATION:

APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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US-09-540-149A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application Patent No. 6511699
                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Escherichia
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 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGCCGTCATGGT
               PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
                                                                        MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla
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Matches:
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CAGATGCGTGATAAAACGCCGCTATCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                      ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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; Sequence 9, Application US/10266041A
; Patent No. 6974690
; GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVI-
FILE REFERENCE: 19603/2798
; CURRENT APPLICATION NUMBER: US/10/266,041A
CURRENT TILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR APPLICATION NUMBER: 09/203-31
PRIOR PILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEG ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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Best Local Similarity:
Query Match:
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TYPE: DNA
ORGANISM: Escherichia
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AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180
                                                   SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160
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                                                                                                          GCCTTCGCCGCCGGGCTGGCACCTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                                                                                                                                                CAGCCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENES
FILE REFERENCE: 19603/4031
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1486
TYPE: DNA
ORGANISM: Escherichia coli
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US-09-715-477-4
; Sequence 4, Application
; Patent No. 6841370
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                                                   ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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US-08-910-798-1
Alignment Scores:
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                                                                                                                                TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS; double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08910798
Patent No. 5876997
GENERAL INFORMATION:
APPLICANT: KRETZ
TITLE OF INVENTION: NOVEL PHYTAL
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                   MOLECULE TYPE: DNA (genomic)
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CORRESPONDENCE ADDRESS:
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                                                                     ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
                                                                                                                 GlyGlyGluLeuIleAlaTyrLeuGlyHisTyrTrpArgGlnArgLeuValAlaAspGly
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     LeuLeuProLysCysGlyCysProGlnSerGlyGlnValAlaIleIleAlaAspValAsp 112
                                                                                                                                                                                                                                      AspValThrProAspAlaTrpProThrTrpProValLysLeuGlyGluLeuThrProArg
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                                                                                                                                                                                                                                                                                      GCTTCGCTGCTCACCGCCTGGACTTTAAGCCCTATCAACTGCCCGGCCAGTATGAGCGC 1029
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GACCAGGGATTCTGCCCGCTGGAGACCTTTAAAATGGTGATCAACGAGGCG
                                 AlaGlnGlyMetCysSerLeuAlaGlyPheThrGlnIleValAsnGluAla 425
                                                                                                     SerLeuAsnThrProProGlyGluValLysLeuThrLeuAlaGlyCysGluGluArgAsn 408
                                                                                                                                                                             TrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArgAspLysThrProLeu 388
                                                                                                                                                                                                                                                                                                                     AlaAsnLeuGlyGlyAlaLeuGluLeuAsn---TrpThrLeuProGlyGlnProAspAsn
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                                                                       ACCCTGCAGGCCCCGCCGCAGCGGGTCACTCTGGCGCTTAACGGCTGTCCGGTT---GAT
                                                                                                                                            CTGATGAAGATTGAGTATGTCTATCAAAGTACCGAGCAACTGCGTAACGCCGACGCGTTA 1149
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Search completed: June 14, 2006, 15:34:57 Job time : 248.459 secs

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CTGGTGACCAGCGGCGAGTGCCCGCCGGAAAACGCGGTTTATGCCTACGCTAACAGCCTG

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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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US-11-05-354-2
US-10-156-660-2
US-09-866-379-10
US-09-866-379-8
US-10-1601-319-8
US-10-601-319-8
US-10-601-319-8
US-10-933-115-8
US-11-018-709-1
US-10-933-115-8
US-11-018-709-2
US-10-933-115-2
US-10-334-672-1
US-10-334-672-1
US-10-334-672-1
US-10-021-723A-13
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US-10-021-723A-13
US-10-021-723A-13
US-10-021-723A-15
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                                                  Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 15, Appli Seque
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US-10-601-319-10
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197	197	197	310	414	462.5	475.5	627.5	637	782	948.5	951.5	959.5	976.5	1192	2112	2144	2147
8.7	8.7	8.7	13.7	18.3	20.5	21.1	27.8	28.2	34.6	42.0	42.1	42.5	43.2	52.8	93.5	95.0	95.1
426	426	426	118	441	421	409	318	144	476	420	441	441	441	261	432	432	433
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US-10-450-763-53707	US-10-343-357-6	US-10-257-174-44	US-10-450-763-56055	US-11-098-686-10683	US-10-021-723A-6	US-10-021-723A-8	US-10-021-723A-14	US-10-450-763-54615	US-10-021-723A-10	US-10-021-723A-4	US-10-021-723A-2	US-10-282-122A-77792	US-10-021-723A-12	US-10-450-763-56057	US-10-021-723A-16	US-10-284-962-5	US-10-266-041-1
53	Sequence 6, Appli	Sequence 44, Appl	Sequence 56055, A	Sequence 10683, A	Sequence 6, Appli	Sequence 8, Appli	Sequence 14, Appl	Sequence 54615, A	Sequence 10, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 77792, A	Sequence 12, Appl	Sequence 56057, A	Sequence 16, Appl	Sequence 5, Appli	Sequence 1, Appli

ALIGNMENTS

Application US/10601319 US20040091968A1

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APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
FILE REFERENCE: 09010-029011
CURRENT PILING DATE: 2001-029011
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
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APPLICANT: Kretz, Keith A.
APPLICANT: Kretz, Keith A.
APPLICANT: Barton, Nelson Ro
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Eile
APPLICANT: Mathur, Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 10
                                                                                                                                                                                                                                     Query Match 100.0%; Score 2258; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-196; Matches 432; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: modified phytase enzyme
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                                                                                                                 Length 432;
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PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR PILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PRILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEC ID NO 10
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US-10-933-115-10
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                                                                                                                                                        ; OTHER INFORMATION: modified phytase enzyme
US-10-933-115-10
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                                                                             Matches
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APPLICANT:
                                                                                                               Query Match
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APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT FILING DATE: 2004-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Short, Jay M. APPLICANT: Kretz, Keith A. APPLICANT: Gray, Kevin A.
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                              FEATURE:
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432; Conser
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                                                                         100.0%; Score 2258; DB 5; larity 100.0%; Pred. No. 1.8e-196; Conservative 0; Mismatches 0;
                                                                                                                 Length 432;
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APPLICANT: SHORT, Jay M.
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Kevin A.
APPLICANT: GRAY, Kevin A.
APPLICANT: GARRETY, James B.
APPLICANT: GARRETY, James B.
APPLICANT: MATHUR, Eric J.
ITILE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THE
ITITLE OF INVENTION NUMBER: US/11/056,354
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 10/156,660
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
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                                                                                                                     US-11-056-354-2
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                                                                                                                                                                                                 SOPTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 432; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/11056354
Publication No. US20050246780A1
                                                                                                                                                                               FEATURE:
                                                                                                                                              INFORMATION: Modified phytase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIFLLQQAQCMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA 300
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Score 2258; DB 6;
Pred. No. 1.8e-196;
); Mismatches 0;
                                                         Length
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Gaps

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Sequence 2. Application US/10156660
Publication No. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Short, Jay M.
APPLICANT: Gary, Kevin A.
APPLICANT: Gary, Kevin A.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCITILE OF INVENTION: AND METHODS FOR MAKING AND FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US/10/156,660
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/292,214
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 09/299,214
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/299,214
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
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PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
; OTHER INFORMATION: modified phytase enzyme US-10-156-660-2
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US-10-156-660-2
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                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                  ENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
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APPLICANT: GARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/21,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified phytase
US-09-866-379-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-866-379-10
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                                                                                             NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US2002013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09866379 Patent No. US20020136754A1
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Matches 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
                                                                                  TYPE: PRT
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Pred. No. 1.8e-196;
D; Mismatches 0;
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APPLICANT: MINTANANA CONTROL SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
APPLICANT: O'DONOGHUE, EILEEN
CURRENT FILLE OF INVENTION NUMBER: US/9/866,379
CURRENT APPLICATION NUMBER: US 9/580,515
PRIOR APPLICATION NUMBER: US 99/580,515
PRIOR FILLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 432
TYPE: PRT
                                                        ; TYPE: PRT ; ORGANISM: Escherichia coli US-09-866-379-8
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US-09-866-379-8
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Query Match
Best Local Similarity
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
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98.1%;
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 Score 2182; DB 3; Pred. No. 1.5e-189;
                   Length 432;
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     Query Match
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; TYPE: PRT
; ORGANISM: Be
US-10-156-660-4
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
APPLICANT: Garrett, James
APPLICANT: O'Donoghue, Bi
                                                                                                                                                                                                                                                                                                           APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: AND METHODS FOR MAKING AND METHODS FOR MAKING AND FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US/10/156,660
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/80,515
PRIOR APPLICATION NUMBER: US 09/80,515
PRIOR APPLICATION NUMBER: US 09/80,515
PRIOR APPLICATION NUMBER: US 09/318,528
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US-10-156-660-4
                                                                                                                                PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
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                                                               SOPTWARE: FASTSEQ
SEQ ID NO 4
LENGTH: 432
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96.6%;

Score

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Length

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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE; ELITEA.034A; CURRENT APPLICATION NUMBER: US/10/282,122A; CURRENT FILING DATE: 2000-02-20; PRIOR APPLICATION NUMBER: 60/191,078; PRIOR APPLICATION NUMBER: 60/206,848; PRIOR PILING DATE: 2000-05-23; PRIOR FILING DATE: 2000-05-23; PRIOR APPLICATION NUMBER: 60/207,727; PRIOR FILING DATE: 2000-05-26; PRIOR FILING DATE: 2000-05-26; PRIOR FILING DATE: 2000-09-06; PRIOR APPLICATION NUMBER: 60/230,335; PRIOR APPLICATION NUMBER: 60/230,337; PRIOR APPLICATION NUMBER: 60/230,347; PRIOR APPLICATION NUMBER: 60/230,347; PRIOR APPLICATION NUMBER: 60/242,578; PRIOR APPLICATION NUMBER: 60/253,625; PRIOR APPLICATION NUMBER: 60/257,931
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        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Yamamoto, Ro
Forsyth, R.
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Wall, Daniel
Trawick, John
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Malone, Cheryl
Haselbeck, Robert
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lio, Carlos
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APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES ANI
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43351
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application Publication No. US200400
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Best Local
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Pred. No. 1.5e-189;
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300

240

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240

180

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120

60

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GENERAL INFORMATION:
APPLICANT: Cargill, Incorporated
ITILE OF INVENTION: Myo-Inssitol Oxygenases
FILE REFERENCE: 10829/003US1
CURRENT APPLICATION NUMBER: US/10/472,317
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/US02/08404
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
VOUNDER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PRIOR APPLICATION NUMBER: US 09/291,931; PRIOR FILING DATE: 1999-04-13; PRIOR APPLICATION NUMBER: US 09/259,214; PRIOR FILING DATE: 1999-03-01; PRIOR APPLICATION NUMBER: US 08/910,798; PRIOR FILING DATE: 1997-08-13; NUMBER OF SEQ ID NOS: 10; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 8
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US-10-472-317-41
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; TYPE: PRT
; ORGANISM: Escherichia
US-10-601-319-8
                                                                                                                                                                                                                                                                                              Sequence 41, Application US/10472317 Publication No. US20040185562A1
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Best Local Similarity
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            LENGTH: 432
TYPE: PRT
ORGANISM: Escherichia coli
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Pred. No. 1.5e-189;
0; Mismatches 8;
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APPLICANT: Garrett, James B.

APPLICANT: O' DONOghue, Eileen
APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/9/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US/9/866,379
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US/9/318,528
PRIOR APPLICATION NUMBER: US/9/318,528
PRIOR APPLICATION NUMBER: US/9/311,931
PRIOR APPLICATION NUMBER: US/9/291,931
; TYPE: PRT ; ORGANISM: Escherichia US-10-933-115-8
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US-10-933-115-8
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Publication No. US20050281792A1
                                                                       SEQ ID NO 8
LENGTH: 4:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
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                                                                                                                         Version 4.0
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Pred. No. 1.5e-189;
0; Mismatches 8;
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APPLICANT: GRAT, REVII A.

APPLICANT: GARRETT, James B.

APPLICANT: GONOGHUE, Eileen

APPLICANT: O'DONOGHUE, Eileen

APPLICANT: O'DONOGHUE, Eileen

APPLICANT: O'DONOGHUE, Eileen

TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM AND

TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM

FILE REFERENCE: 564462001803/D1370-901

CURRENT PILLING DATE: 2005-02-11

PRIOR APPLICATION NUMBER: US 10/156,660

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/80,515

PRIOR APPLICATION NUMBER: US 09/80,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

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US-11-056-354-4
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APPLICANT:
APPLICANT:
APPLICANT:
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Pred. No. 1.5e-189;
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Sequence 1, Application US/11018709
Publication No. US20050095691A1
GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/11/018,709
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: US/9/715,477
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR PILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 432
TYPE: PRI
TYPE: PRI
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US-11-018-709-1
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; ORGANISM: Escherichia coli appA phytase
US-11-056-354-4
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Best Local
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Matches 42
                                                                                                                                                                                                                                                                                                                           ORGANISM: Escherichia
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ilarity 97.9%;
Conservative
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ilarity 98.1%;
Conservative
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                                                                                                                                                                                     Score 2177; DB 6;
Pred. No. 4.3e-189;
0; Mismatches 9;
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Pred. No. 1.5e-189;
0; Mismatches 8;
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PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR PRIOR PRIOR NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTMARE: PatentIn version 3.0
SEQ ID NO 2
ILENCTU- 1.
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                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n is any nucleotide
US-09-777-566A-2
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US-09-777-566A-2
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                                                                                                                                                                                                                              Matches 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-6
CURRENT APPLICATION NUMBER: US/09/777,566A
CURRENT FILING DATE: 2001-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DIVERSA CORPORATION APPLICANT: SHORT, Jay APPLICANT: KRETZ, Keith
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Escherichia
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 440
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                                                                                  TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR TILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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US-09-866-379-2
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                                                                                                                                                                                                                                                                                                        Query Match
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TYPE: PRT
ORGANISM: Escherichia coli
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                                              AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH 180
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360	LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPPGGELVFERW 360	301	망
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300	TDSHQWNTLLSLHNAQFYLLQRTPEVARSRA	241	망
300	EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA 300	241	\$
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